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# OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 18:59:56 ; Search time 560 Seconds  
(without alignments)  
9284.622 Million cell updates/sec

Title: US-10-763-854-1

Perfect score: 1014

Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

## Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*

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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1014	100.0	1014	US-10-023-775B-1	Sequence 1, Appli
2	1014	100.0	1014	US-10-278-141-10	Sequence 10, Appl
3	1014	100.0	1014	US-10-296-081-10	Sequence 10, Appl
4	1014	100.0	1014	US-10-763-854-1	Sequence 1, Appli
5	1014	100.0	1560	US-10-023-634-5	Sequence 5, Appli
6	1014	100.0	1851	US-10-055-569A-7	Sequence 3, Appli
7	1012.4	99.8	1014	US-09-943-798-3	Sequence 3, Appli
8	1012.4	99.8	1014	US-09-885-453-2	Sequence 2, Appli
9	1012.4	99.8	1014	US-10-270-144-1	Sequence 7, Appli
10	1012.4	99.8	1014	US-10-188-405-7	Sequence 7, Appli
11	1012.4	99.8	1014	US-10-079-384-13	Sequence 13, Appl
12	1012.4	99.8	1014	US-10-225-567A-646	Sequence 646, App

## ALIGNMENTS

RESULT 1

US-10-023-775B-1

; Sequence 1, Application US/10023775B

; Publication No. US2003002282A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc. (EP/GB) only

; APPLICANT: Pfizer Inc. (US, JP, EB except GB)

; APPLICANT: Fidcock, Mark David

; TITLE OF INVENTION: No. US2003002282A1 Polypeptide

; FILE REFERENCE: PC10959AGPR

; CURRENT APPLICATION NUMBER: US/10/023,775B

; CURRENT FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: GB 0030854.4

; PRIOR FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: US 60/260,590

; PRIOR FILING DATE: 2001-01-09

; PRIOR APPLICATION NUMBER: US 60/296,660

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: GB 0111031.1

; PRIOR FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1014

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-023-775B-1

Query Match 100.0%; Score 1014; DB 14; Length 1014;

Best Local Similarity 100.0%; Pred. No. 5.3e-294;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATCAGCTGCT 60

DB 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATCAGCTGCT 60

Sequence 27, Appli

Sequence 5, Appli

Sequence 13, Appli

Sequence 27, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 525, App

Sequence 463, App

Sequence 3, Appli

Sequence 17, Appli

Sequence 85, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 59, Appli

Sequence 40, Appli

Sequence 102, Appli

Sequence 4, Appli

Sequence 104, App

Sequence 218, Appli

Sequence 1, Appli

Sequence 1456, Ap

Sequence 35, Appli

Sequence 37, Appli

Sequence 35, Appli

Sequence 35, Appli

Sequence 37, Appli

Sequence 35, Appli

Sequence 566, App

Sequence 36, Appli

Sequence 36, Appli

Sequence 1352, Ap

QY 61 TTTGAAATTCAGCTGATGAAACATCCCACTCAAGATGCATCTCCCTGTTATTAT 120  
DB 61 TTTGAAATTCAGCTGATGAAACATCCCACTCAAGATGCATCTCCCTGTTATTAT 120  
QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGAGTAGTATCACTTACATTTTC 180  
DB 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGAGTAGTATCACTTACATTTTC 180  
QY 181 AAAATGAGACCTTGAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATCTG 240  
DB 181 AAAATGAGACCTTGAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATCTG 240  
QY 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACCTGGATC 300  
DB 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACCTGGATC 300  
QY 301 TTTGAGATTTTCAATGTAAGTTTATCCGCTTCAGCTTCCTCAATTCACCTGTATAGCAGC 360  
DB 301 TTTGAGATTTTCAATGTAAGTTTATCCGCTTCAGCTTCCTCAATTCACCTGTATAGCAGC 360  
QY 361 ATCCCTTCTTCCCTCAGCTGTTTCAAGCATCTTCGCTACTGCTGATCATTCACCCATGAGC 420  
DB 361 ATCCCTTCTTCCCTCAGCTGTTTCAAGCATCTTCGCTACTGCTGATCATTCACCCATGAGC 420  
QY 421 TGCTTTTCCATTCACAAAACCTCGATGTGCGAGTGTAGCTGTGCTGTGCTGTGATCAAT 480  
DB 421 TGCTTTTCCATTCACAAAACCTCGATGTGCGAGTGTAGCTGTGCTGTGCTGTGATCAAT 480  
QY 481 TCATGTTAGTGTGCTATTCGAGTACCTTTTGTATCAATCAACAGGACCAACAGA 540  
DB 481 TCATGTTAGTGTGCTATTCGAGTACCTTTTGTATCAATCAACAGGACCAACAGA 540  
QY 541 TCAGCTGTCTGAGCTCAGCTCAGGATTCGAGTGAACCTCAATCAATTAAGTGGTACACCTA 600  
DB 541 TCAGCTGTCTGAGCTCAGGATTCGAGTGAACCTCAATCAATTAAGTGGTACACCTA 600  
QY 601 ATTTTGAAGTCAACTACTTTTCCCTTCCCTTGGTATGATGACACTTTGCTATACGAG 660  
DB 601 ATTTTGAAGTCAACTACTTTTCCCTTCCCTTGGTATGATGACACTTTGCTATACGAG 660  
QY 661 ATTATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720  
DB 661 ATTATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720  
QY 721 AGGCTAAACCATCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 780  
DB 721 AGGCTAAACCATCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 780  
QY 781 AGGGTCATTCGGATCGAATCTCGCTTCCCTTCAATCAGTGTGTTCCATTCAGAAATCAGATC 840  
DB 781 AGGGTCATTCGGATCGAATCTCGCTTCCCTTCAATCAGTGTGTTCCATTCAGAAATCAGATC 840  
QY 841 CATGAAGCTTACATGCTTCTAGACCATGATGCTGCTGAAACACTTTGGTAACTGTTA 900  
DB 841 CATGAAGCTTACATGCTTCTAGACCATGATGCTGCTGAAACACTTTGGTAACTGTTA 900  
QY 901 CTATATGCTGCTGAGCAGCAACTTTTCAAGAGGCTGCTGCTCAACAGTGAATGCAAA 960  
DB 901 CTATATGCTGCTGAGCAGCAACTTTTCAAGAGGCTGCTGCTCAACAGTGAATGCAAA 960  
QY 961 GTAAGCGGAACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014  
DB 961 GTAAGCGGAACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

## RESULT 2

US-10-278-141-10  
; Sequence 10, Application US/10278141  
; Publication No. US20030138818A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: LU, Dyoung Aina M.

; APPLICANT: THORNTON, Michael  
; APPLICANT: LU, Yan  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: GRAUL, Richard  
; APPLICANT: KHAN, Farrah A.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: NGUYEN, Damiel B.  
; APPLICANT: YUE, Henry  
; APPLICANT: HAFALIA, April  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: LAL, Preeti  
; APPLICANT: REDDY, Roopa  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AU-YOUNG, Janice  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0096 USA  
; CURRENT APPLICATION NUMBER: US/10/278,141  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: 60/208,834  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/207,566  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: US01/16285  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 60/205,628  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: 60/208,861  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/206,222  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PERL Program  
; SEQ ID NO 10  
; LENGTH: 1014  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030138818A1 6575963CB1  
US-10-278-141-10

Query Match 100.0%; Score 1014; DB 15; Length 1014;

Best Local Similarity 100.0%; Pred. No. 5.3e-294;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTTCGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60  
DB 1 ATGAATGAGCCACTAGACTATTTCGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60  
QY 61 TTTGAAATTCAGCTGATGAAACATCCCACTCAAGATGCATCTCCCTGTTATTAT 120  
DB 61 TTTGAAATTCAGCTGATGAAACATCCCACTCAAGATGCATCTCCCTGTTATTAT 120  
QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGAGTAGTATCACTTACATTTTC 180  
DB 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGAGTAGTATCACTTACATTTTC 180  
QY 181 AAAATGAGACCTTGAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATCTG 240  
DB 181 AAAATGAGACCTTGAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATCTG 240  
QY 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACCTGGATC 300  
DB 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACCTGGATC 300  
QY 301 TTTGAGATTTTCAATGTAAGTTTATCCGCTTCAGCTTCCTCAATTCACCTGTATAGCAGC 360  
DB 301 TTTGAGATTTTCAATGTAAGTTTATCCGCTTCAGCTTCCTCAATTCACCTGTATAGCAGC 360  
QY 361 ATCCCTTCTTCCCTCAGCTGTTTCAAGCATCTTCGCTACTGCTGATCATTCACCCATGAGC 420

Db 361 AFCCCTCTCTCACCTGTTTCAGCATCTTCGCTACTGTGTGATCAATTCACCCAAATGAGC 420  
Qy 421 TGCTTTTCCATTCACAAACTCGATGTGAGCTGTGAGCTGTGCTGTGTGGATCATTT 480  
Db 421 TGCTTTTCCATTCACAAACTCGATGTGAGCTGTGAGCTGTGCTGTGTGGATCATTT 480  
Qy 481 TCATGTGTAGTGTGATTCGAGTACCTTCCTGATCACATCAACCAACAGGACCAACAGA 540  
Db 481 TCATGTGTAGTGTGATTCATTCGATGACCTTCCTGATCACATCAACCAACAGGACCAACAGA 540  
Qy 541 TCAGCTGTCTGAGCTCACCACTTCAGTGTGAGTGAATCAATATTAAGTGTGAACCTTA 600  
Db 541 TCAGCTGTCTGAGCTCACCACTTCAGTGTGAGTGAATCAATATTAAGTGTGAACCTTA 600  
Qy 601 ATTTTGACTGCAACTACTTCTGCTCCCTTGGTGTGATGACACTTTGCTATACACAG 660  
Db 601 ATTTTGACTGCAACTACTTCTGCTCCCTTGGTGTGATGACACTTTGCTATACACAG 660  
Qy 661 ATTATCCACACTCTGACCATGGACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720  
Db 661 ATTATCCACACTCTGACCATGGACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720  
Qy 721 AGGCTAACCATCTGCTACTCTTCGATTTTACGATGTTTATACCTTCCATATCTTG 780  
Db 721 AGGCTAACCATCTGCTACTCTTCGATTTTACGATGTTTATACCTTCCATATCTTG 780  
Qy 781 AGGCTCATTCGATCGAATCTCGCTGCTTTCAATCAGTGTGCTCAATGAGAAATCAGATC 840  
Db 781 AGGCTCATTCGATCGAATCTCGCTGCTTTCAATCAGTGTGCTCAATGAGAAATCAGATC 840  
Qy 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGCTGAACCACTTTGGTAACTGTGA 900  
Db 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGCTGAACCACTTTGGTAACTGTGA 900  
Qy 901 CTATATGTGGTGTGAGCAGCAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA 960  
Db 901 CTATATGTGGTGTGAGCAGCAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA 960  
Qy 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTTAGTACTCAACCAACCCCTTGA 1014  
Db 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTTAGTACTCAACCAACCCCTTGA 1014

## RESULT 3

US-10-296-081-10  
; Sequence 10, Application US/10296081  
; Publication No. US20030220477A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: THORNTON, Michael  
; APPLICANT: LU, Yan  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: GRAUL, Richard  
; APPLICANT: KHAN, Farrah A.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: NGUYEN, Daniel B.  
; APPLICANT: YUE, Henry  
; APPLICANT: HAFALIA, April  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: LAL, Preeti  
; APPLICANT: REDDY, Roopa  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AU-YOUNG, Janice  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0096 PCT  
; CURRENT APPLICATION NUMBER: US/10/296,081  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208,861  
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02

; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PERL Program  
; SEQ ID NO 10  
; LENGTH: 1014  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030220477A1 6575963CB1  
US-10-296-081-10

Query Match 100.0%; Score 1014; DB 15; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 5.3e-294;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTTCCCGATTAATGACAGTGT 60  
Db 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTTCCCGATTAATGACAGTGT 60  
Qy 61 TTTGGAAATTTGCACATGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
Db 61 TTTGGAAATTTGCACATGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
Qy 121 GGCATTATCTTCTCTGCTGGATTTCCAGGCAATGCAAGTAGTGATATCCACTTTACATTTTC 180  
Db 121 GGCATTATCTTCTCTGCTGGATTTCCAGGCAATGCAAGTAGTGATATCCACTTTACATTTTC 180  
Qy 181 AAATGAGACCTTGAAGAGAGAGACCAATCATTTATGCTGAACCTGGCTGCAAGATCTG 240  
Db 181 AAATGAGACCTTGAAGAGAGAGACCAATCATTTATGCTGAACCTGGCTGCAAGATCTG 240  
Qy 241 CTGTATCTGACAGCTCCCTTCTGATTCACATCTATGCGAGTGGCGAAACCTGGATC 300  
Db 241 CTGTATCTGACAGCTCCCTTCTGATTCACATCTATGCGAGTGGCGAAACCTGGATC 300  
Qy 301 TTTGGAGATTTTCATGTGAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Db 301 TTTGGAGATTTTCATGTGAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Qy 361 ATCTCTTCTCAGCTGTTTCCAGCATCTTCGCTACTGTGTGATCATTCACCCAAATGAGC 420  
Db 361 ATCTCTTCTCAGCTGTTTCCAGCATCTTCGCTACTGTGTGATCATTCACCCAAATGAGC 420  
Qy 421 TGCTTTTCCATTCACAAACTCGATGTGAGCTGTGAGCTGTGCTGTGTGGATCATTT 480  
Db 421 TGCTTTTCCATTCACAAACTCGATGTGAGCTGTGAGCTGTGCTGTGTGGATCATTT 480  
Qy 481 TCATGTGTAGTGTCAATTCGATGACCTTTCTTGATCACATCAACCAACAGGACCAACAGA 540  
Db 481 TCATGTGTAGTGTCAATTCGATGACCTTTCTTGATCACATCAACCAACAGGACCAACAGA 540  
Qy 541 TCAGCTGTCTGAGCTCACCACTCACAGTTCGGATGAACCTCAATATTAAGTGTGAACCTTA 600  
Db 541 TCAGCTGTCTGAGCTCACCACTCACAGTTCGGATGAACCTCAATATTAAGTGTGAACCTTA 600  
Qy 601 ATTTTGACTGCAACTACTTCTGCTCCCTTGGTGTGATGACACTTTGCTATACACAG 660  
Db 601 ATTTTGACTGCAACTACTTCTGCTCCCTTGGTGTGATGACACTTTGCTATACACAG 660  
Qy 661 ATTATCCACACTCTGACCATGGACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720  
Db 661 ATTATCCACACTCTGACCATGGACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720  
Qy 721 AGGCTAACCATCTGCTACTCTTCGATTTTACGATGTTTATACCTTCCATATCTTG 780  
Db 721 AGGCTAACCATCTGCTACTCTTCGATTTTACGATGTTTATACCTTCCATATCTTG 780  
Qy 781 AGGCTCATTCGATCGAATCTCGCTGCTTTCAATCAGTGTGCTCAATGAGAAATCAGATC 840  
Db 781 AGGCTCATTCGATCGAATCTCGCTGCTTTCAATCAGTGTGCTCAATGAGAAATCAGATC 840  
Qy 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGCTGAACCACTTTGGTAACTGTGA 900  
Db 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGCTGAACCACTTTGGTAACTGTGA 900

Db 841 CATGAAGCTTACATCGTTTCTAGACCAATTAGTCTCTGAACACCTTTGGTAACTGTGA 900  
Qy 901 CTATATGCTGGTTCAGGCACTTTTCAGAGGCTCTGCTCAACAGTGAAGTCAAA 960  
Db 901 CTATATGCTGGTTCAGGCACTTTTCAGAGGCTCTGCTCAACAGTGAAGTCAAA 960  
Qy 961 GTAAAGCGGGAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACACCTTTGA 1014  
Db 961 GTAAAGCGGGAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACACCTTTGA 1014

## RESULT 4

US-10-763-854-1  
; Sequence 1, Application US/10763854  
; Publication No. US2004013757A1  
; GENERAL INFORMATION:  
; APPLICANT: PFIZER INC.  
; TITLE OF INVENTION: Novel Polypeptide  
; FILE REFERENCE: PC10959B  
; CURRENT APPLICATION NUMBER: US/10/763,854  
; CURRENT FILING DATE: 2004-01-22  
; PRIOR APPLICATION NUMBER: GB 0030854.4  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 10/023,775  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/296,660  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/260,590  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: GB 0111031.1  
; PRIOR FILING DATE: 2001-05-04  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 1  
; LENGTH: 1014  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-763-854-1

Query Match 100.0%; Score 1014; DB 17; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 5.3e-294;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGATTATGCACTGCT 60  
Db 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGATTATGCACTGCT 60  
Qy 61 TTTGGAAATTCAGTGAATGCAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120  
Db 61 TTTGGAAATTCAGTGAATGCAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120  
Qy 121 GGCATTATCTCTGCTGGGATTTCCAGGGAATGCAAGTGAATGATATCCACTATTTTC 180  
Db 121 GGCATTATCTCTGCTGGGATTTCCAGGGAATGCAAGTGAATGATATCCACTATTTTC 180  
Qy 181 AAAATGAGACCTTGAAGAGAGACCACTATTATGCTGAACCTGGCTGCACAGATCTG 240  
Db 181 AAAATGAGACCTTGAAGAGAGACCACTATTATGCTGAACCTGGCTGCACAGATCTG 240  
Qy 241 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTATGCGAGTGGCGGAAACTGGATC 300  
Db 241 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTATGCGAGTGGCGGAAACTGGATC 300  
Qy 301 TTTGAGATTTTCATGTGAAGTTTATCCGCTTCAGCTTCCATTTCAACTGTATAGCAG 360  
Db 301 TTTGAGATTTTCATGTGAAGTTTATCCGCTTCAGCTTCCATTTCAACTGTATAGCAG 360  
Qy 361 ATCTCTTCTCCACTGTTTTCAGCATCTTCGCTACTGTGTGATCATTCACCCATGAGC 420  
Db 361 ATCTCTTCTCCACTGTTTTCAGCATCTTCGCTACTGTGTGATCATTCACCCATGAGC 420  
Qy 421 TGTCTTTCCATTACAAAACTCGATGTCAGTTGTAGCCTGTGCTGTGTGGTGGATCAT 480

Db 421 TGTCTTTCCATTACAAAACTCGATGTCAGTTGTAGCCTGTGCTGTGGTGGATCAT 480  
Qy 481 TCACTGTAGTGTCTCATTCGATGACCTTTCTTGATACATCAACCAACAGACCAACAGA 540  
Db 481 TCACTGTAGTGTCTCATTCGATGACCTTTCTTGATACATCAACCAACAGACCAACAGA 540  
Qy 541 TCAGCCTGTCTCGACCTCACCCAGTTCGGATGAACCTCAATACTATTAAAGTGTGTAACACCTA 600  
Db 541 TCAGCCTGTCTCGACCTCACCCAGTTCGGATGAACCTCAATACTATTAAAGTGTGTAACACCTA 600  
Qy 601 ATTTTGACTGCAACTACTTTCTGCTCCCTTGGTGTAGTGAACACTTTTGTATACACAG 660  
Db 601 ATTTTGACTGCAACTACTTTCTGCTCCCTTGGTGTAGTGAACACTTTTGTATACACAG 660  
Qy 661 ATTATCCACACTCTGACCCATGGAACCTGCAAGTGCCTTAAGCAAAAGCAGCA 720  
Db 661 ATTATCCACACTCTGACCCATGGAACCTGCAAGTGCCTTAAGCAAAAGCAGCA 720  
Qy 721 AGGCTAAACCAATTCCTGCTACTCTTGCATTTTACGTATGTTTTTACCCTTCCATATCTTG 780  
Db 721 AGGCTAAACCAATTCCTGCTACTCTTGCATTTTACGTATGTTTTTACCCTTCCATATCTTG 780  
Qy 781 AGGCTCAATTCGGATCGAAATCTCGCTGCTTCAATCAGTTGTTCCATGAGAATCAGATC 840  
Db 781 AGGCTCAATTCGGATCGAAATCTCGCTGCTTCAATCAGTTGTTCCATGAGAATCAGATC 840  
Qy 841 CATGAAGCTTACATCGTTTCTAGACCAATTAGTCTCTGAACACCTTTGGTAACTGTGA 900  
Db 841 CATGAAGCTTACATCGTTTCTAGACCAATTAGTCTCTGAACACCTTTGGTAACTGTGA 900  
Qy 901 CTATATGCTGGTTCAGGCACTTTTCAGAGGCTCTGCTCAACAGTGAAGTCAAA 960  
Db 901 CTATATGCTGGTTCAGGCACTTTTCAGAGGCTCTGCTCAACAGTGAAGTCAAA 960  
Qy 961 GTAAAGCGGGAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACACCTTTGA 1014  
Db 961 GTAAAGCGGGAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACACCTTTGA 1014

## RESULT 5

US-10-023-634-5  
; Sequence 5, Application US/10023634  
; Publication No. US2003023638A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkete, Richard A  
; APPLICANT: Colman, Steven D  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Ballinger, Robert A  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Li, Li  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Zerkhusen, Bryan D  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gangoli, Esha A  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Gunther, Erik  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Gerlach, Valerie  
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
; FILE REFERENCE: 21402-221  
; CURRENT APPLICATION NUMBER: US/10/023,634  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/256,025



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/ PRIOR FILING DATE: 2000-12-15
/ PRIOR APPLICATION NUMBER: 60/265,163
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,929
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/274,864
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/276,688
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,880
/ PRIOR FILING DATE: 2001-03-22
/ PRIOR APPLICATION NUMBER: 60/286,409
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: 60/309,246
/ PRIOR FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: 60/315,600
/ PRIOR FILING DATE: 2001-08-29
/ NUMBER OF SEQ ID NOS: 132
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 1560
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-023-634-5

Query Match          100.0%; Score 1014; DB 15; Length 1560;
Best Local Similarity 100.0%; Pred. No. 6.8e-294;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTCAGCTGCT 60
DB 353 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTCAGCTGCT 412
QY 61 TTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
DB 413 TTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 472
QY 121 GCAATTATCTTCTCGTGGGATTTCCAGGCAATGCAATGATGATATCCACTTACATTTTC 180
DB 473 GCAATTATCTTCTCGTGGGATTTCCAGGCAATGCAATGATGATATCCACTTACATTTTC 532
QY 181 AAAATGAGACCTTGAAGAGCAGCACCACATCATTTATGCTGAACCTGGCTGCAAGATCTG 240
DB 533 AAAATGAGACCTTGAAGAGCAGCACCACATCATTTATGCTGAACCTGGCTGCAAGATCTG 592
QY 241 CTGTATCTGACGAGCTCCCTTCTGATTCATCTACTATGCCAGTGGCGAAAACCTGGATC 300
DB 593 CTGTATCTGACGAGCTCCCTTCTGATTCATCTACTATGCCAGTGGCGAAAACCTGGATC 652
QY 301 TTGAGAGATTTTCATGTTGAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGCAGC 360
DB 653 TTGAGAGATTTTCATGTTGAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGCAGC 712
QY 361 ATCTCTTCTCCTCACCTGTTTACGATCTTCCGCTACTGTTGATCATTCACCCAAATGAGC 420
DB 713 ATCTCTTCTCCTCACCTGTTTACGATCTTCCGCTACTGTTGATCATTCACCCAAATGAGC 772
QY 421 TGTCTTTCCATTCACAAACTCGATGTCAGTTGAGTTGAGCTTGTGCTGTGTGGATCATTT 480
DB 773 TGTCTTTCCATTCACAAACTCGATGTCAGTTGAGTTGAGCTTGTGCTGTGTGGATCATTT 832
QY 481 TCACCTGGTGTGCTCATTCGAGTACCTTCTTGATCACATCAACCAAGGACCAACAGA 540
DB 833 TCACCTGGTGTGCTCATTCGAGTACCTTCTTGATCACATCAACCAAGGACCAACAGA 892
QY 541 TCAGCTGTCTCGACCTACCACTCCAGTTCCGATGAACCTCAATTAATTAAGTGGTACACCTTA 600
DB 893 TCAGCTGTCTCGACCTACCACTCCAGTTCCGATGAACCTCAATTAATTAAGTGGTACACCTTA 952
QY 601 ATTTTGACTGCAACTACTTTTCTGCTCCCTTGGTGATAGTGACACTTTTGTCTATACCG 660
DB 953 ATTTTGACTGCAACTACTTTTCTGCTCCCTTGGTGATAGTGACACTTTTGTCTATACCG 1012
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QY 661 ATTATCCACACTCTGACCCACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCACGA 720
DB 1013 ATTATCCACACTCTGACCCACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCACGA 1072
QY 721 AGGCTAACCAATTCCTGCTACTCTCTGCAATTTTACGATATGTTTTTACCTTCCATATCTTG 780
DB 1073 AGGCTAACCAATTCCTGCTACTCTCTGCAATTTTACGATATGTTTTTACCTTCCATATCTTG 1132
QY 781 AGGCTCATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTCAGATCAGATC 840
DB 1133 AGGCTCATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTCAGATCAGATC 1192
QY 841 CATGAAGCTTACATCGTTTCTAGACCATTTAGCTGCTCTGAAACACCTTTGGTAACTGTTA 900
DB 1193 CATGAAGCTTACATCGTTTCTAGACCATTTAGCTGCTCTGAAACACCTTTGGTAACTGTTA 1252
QY 901 CTATATGTTGGTGTGCTGAGGACAACTTTTTCAGAGGCTGCTGCTCAACAGTGAAGTCAAA 960
DB 1253 CTATATGTTGGTGTGCTGAGGACAACTTTTTCAGAGGCTGCTGCTCAACAGTGAAGTCAAA 1312
QY 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
DB 1313 GTAAGCGGGAACCTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1366
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## RESULT 6

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US-10-055-569A-7
/ Sequence 7, Application US/10055569A
/ Publication No. US20040024181A1
/ GENERAL INFORMATION:
/ APPLICANT: Gangolli, Esha A
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Gilbert, Jennifer
/ APPLICANT: Casman, Stacie
/ APPLICANT: Blalock, Angela
/ APPLICANT: Li, Li
/ APPLICANT: Vernet, Corine
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Mishra, Vishnu S
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Malyanker, Uriel
/ APPLICANT: Stone, David
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Smithson, Glennda
/ APPLICANT: Gunther, Erik
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Taupier Jr., Raymond J
/ APPLICANT: Anderson, David W
/ TITLE OF INVENTION: No. US20040024181A1el Human Proteins, Polynucleotides Encoding The
/ FILE REFERENCE: 21402-191
/ CURRENT APPLICATION NUMBER: US/10/055,569A
/ PRIOR FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: 60/243,642
/ PRIOR FILING DATE: 2000-10-26
/ PRIOR APPLICATION NUMBER: 60/243,320
/ PRIOR FILING DATE: 2000-10-26
/ PRIOR APPLICATION NUMBER: 60/243,592
/ PRIOR FILING DATE: 2000-10-26
/ PRIOR APPLICATION NUMBER: 60/243,681
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: 60/243,863
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: 60/244,443
/ PRIOR FILING DATE: 2000-10-31
/ PRIOR APPLICATION NUMBER: 60/245,029
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: 60/244,995
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: 60/245,293
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;; PRIOR FILING DATE: 2000-11-02  
;; PRIOR APPLICATION NUMBER: 60/245,315  
;; PRIOR FILING DATE: 2000-11-02  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 137  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 7  
;; LENGTH: 1851  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-055-569A-7

Query Match 100.0%; Score 1014; DB 16; Length 1851;  
Best Local Similarity 100.0%; Pred. No. 7.5e-294;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 60  
Db 347 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 406  
Qy 61 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTAT 120  
Db 407 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTAT 466  
Qy 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCACTTACATTTTC 180  
Db 467 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCACTTACATTTTC 526  
Qy 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCCCTGACAGATCTG 240  
Db 527 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCCCTGACAGATCTG 586  
Qy 241 CTGTATCTGACGAGCTCCCTTCTGATTCATCACTATGCGAGTGGGGAACCTGGATC 300  
Db 587 CTGTATCTGACGAGCTCCCTTCTGATTCATCACTATGCGAGTGGGGAACCTGGATC 646  
Qy 301 TTTCGAGATTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Db 647 TTTCGAGATTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 706  
Qy 361 ATCTCTTCCACACTGTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 420  
Db 707 ATCTCTTCCACACTGTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 766  
Qy 421 TGCTTTTCCATTCACAAACTCGATGTGCACTGTAGCTGTGCTGTGGTGGATCATTT 480  
Db 767 TGCTTTTCCATTCACAAACTCGATGTGCACTGTAGCTGTGCTGTGGTGGATCATTT 826  
Qy 481 TCATCTGTAGTGTCAATTCGATGACCTTCTTGTATCAATCAACCAACAGACCAACAGA 540  
Db 827 TCATCTGTAGTGTCAATTCGATGACCTTCTTGTATCAATCAACCAACAGACCAACAGA 886  
Qy 541 TCAGCTGTCTGACCTCAGCTCAGATCGGATCACTCAATCACTATTAAGTGGTACAACTTA 600  
Db 887 TCAGCTGTCTGACCTCAGCTCAGATCGGATCACTCAATCACTATTAAGTGGTACAACTTA 946  
Qy 601 ATTTTGAATGCAACTACTTCTGCTCCCTTGGTGATGATGACACTTGTCTATACCACG 660  
Db 947 ATTTTGAATGCAACTACTTCTGCTCCCTTGGTGATGATGACACTTGTCTATACCACG 1006  
Qy 661 ATTTTGAATGCAACTACTTCTGCTCCCTTGGTGATGATGACACTTGTCTATACCACG 720  
Db 1007 ATTTTGAATGCAACTACTTCTGCTCCCTTGGTGATGATGACACTTGTCTATACCACG 1066  
Qy 721 AGGCTAACCACTTCTGCTACTCTGCTGATTTTACGATGATTTTACCTTCCATATCTTG 780  
Db 1067 AGGCTAACCACTTCTGCTACTCTGCTGATTTTACGATGATTTTACCTTCCATATCTTG 1126  
Qy 781 AGGCTAACCACTTCTGCTACTCTGCTGATTTTACGATGATTTTACCTTCCATATCTTG 840  
Db 1127 AGGCTAACCACTTCTGCTACTCTGCTGATTTTACGATGATTTTACCTTCCATATCTTG 1186  
Qy 841 CATGAGCTTACATGCTTCTTAGACCAATAGCTGCTCTGACACACTTTGGTAACTCTGTTA 900

Db 1187 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAACCTGTTA 1246  
Qy 901 CTATATGTTGGTGCAGGCAAACTTTTCAGCAGGCTGTCTCTCAACAGTGCAGATGCAAA 960  
Db 1247 CTATATGTTGGTGCAGGCAAACTTTTCAGCAGGCTGTCTCTCAACAGTGCAGATGCAAA 1306  
Qy 961 GTAAGCGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014  
Db 1307 GTAAGCGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1360

RESULT 7  
US-09-943-798-3  
; Sequence 3, Application US/09943798  
; Patent No. US20020065215A1  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Group Limited  
; TITLE OF INVENTION: Polypeptide  
; FILE REFERENCE: QG1021  
; CURRENT APPLICATION NUMBER: US/09/943,798  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 1014  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-943-798-3

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 1.6e-293;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 60  
Db 1 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 60  
Qy 61 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTAT 120  
Db 61 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTAT 120  
Qy 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCACTTACATTTTC 180  
Db 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCACTTACATTTTC 180  
Qy 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCCCTGACAGATCTG 240  
Db 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCCCTGACAGATCTG 240  
Qy 241 CTGTATCTGACGAGCTCCCTTCTGATTCATCACTACTATGCGAGTGGGGAACCTGGATC 300  
Db 241 CTGTATCTGACGAGCTCCCTTCTGATTCATCACTACTATGCGAGTGGGGAACCTGGATC 300  
Qy 301 TTTCGAGATTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Db 301 TTTCGAGATTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Qy 361 ATCTCTTCCACACTGTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 420  
Db 361 ATCTCTTCCACACTGTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 420  
Qy 421 TGCTTTTCCATTCACAAACTCGATGTGCACTGTAGCTGTGCTGTGGTGGATCATTT 480  
Db 421 TGCTTTTCCATTCACAAACTCGATGTGCACTGTAGCTGTGCTGTGGTGGATCATTT 480  
Qy 481 TCATCTGTAGTGTCAATTCGATGACCTTCTTGTATCAATCAACCAACAGACCAACAGA 540  
Db 481 TCATCTGTAGTGTCAATTCGATGACCTTCTTGTATCAATCAACCAACAGACCAACAGA 540  
Qy 541 TCAGCTGTCTGACCTCAGCTCAGATCGGATCACTCAATCACTATTAAGTGGTACAACTTA 600  
Db 541 TCAGCTGTCTGACCTCAGCTCAGATCGGATCACTCAATCACTATTAAGTGGTACAACTTA 600

Qy	601	ATTTTGACTGCAACTACTTTCTGCTCCCTTGGTGATGACACTTTTGGCTATATACCACG	660
Db	601	ATTTTGACTGCAACTACTTTCTGCTCCCTTGGTGATGACACTTTTGGCTATATACCACG	660
Qy	661	ATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGCA	720
Db	661	ATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGCA	720
Qy	721	AGGCTAACCAATTCCTGCTACTCCTTGCATTTTACGTATGTTTTTACCCTTCCATATCTTG	780
Db	721	AGGCTAACCAATTCCTGCTACTCCTTGCATTTTACGTATGTTTTTACCCTTCCATATCTTG	780
Qy	781	AGGCTCAATCGGATCGAATCTCGCGCTGCTTCAATCAATGTTTCCATGAGAAATCAGATC	840
Db	781	AGGCTCAATCGGATCGAATCTCGCGCTGCTTCAATCAATGTTTCCATGAGAAATCAGATC	840
Qy	841	CATGAAGCTTACATCTGTTTTCTAGACCAATTAGCTGCTCTGAACACCTTTGGTAAACCTGTTA	900
Db	841	CATGAAGCTTACATCTGTTTTCTAGACCAATTAGCTGCTCTGAACACCTTTGGTAAACCTGTTA	900
Qy	901	CTATATCTGTTGTTGACGCAAACTTTTCAGCAGGCTGTCTGCTCAACAGTCAGATGCAAA	960
Db	901	CTATATCTGTTGTTGACGCAAACTTTTCAGCAGGCTGTCTGCTCAACAGTCAGATGCAAA	960
Qy	961	GTAAGCGGGAACCTTTGACGACGCAAGAAATTAGTTACTCAACAAACCCCTTGA	1014
Db	961	GTAAGCGGGAACCTTTGACGACGCAAGAAATTAGTTACTCAACAAACCCCTTGA	1014
RESULT 8			
US-09-885-453-2			
; Sequence 2, Application US/09885453			
; Publication No. US20030088080A1			
; GENERAL INFORMATION:			
; APPLICANT: Communi, Didier			
; TITLE OF INVENTION: RECEPTOR GPCRxi10			
; FILE REFERENCE: 9409/2082			
; CURRENT APPLICATION NUMBER: US/09/885,453			
; CURRENT FILING DATE: 2001-06-20			
; PRIOR APPLICATION NUMBER: US 09/885,453			
; PRIOR FILING DATE: 2001-06-21			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 2			
; LENGTH: 1014			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: DNA nucleotide sequence			
; LOCATION: (1)..(1014)			
; OTHER INFORMATION: GPCRxi10 DNA sequence			
US-09-885-453-2			
Query Match 99.8%; Score 1012.4; DB 10; Length 1014;			
Best Local Similarity 99.9%; Pred. No. 1.6e-293;			
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATATGCAAGCTGCT	60
Db	1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATATGCAAGCTGCT	60
Qy	61	TTTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGGTTATTAT	120
Db	61	TTTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGGTTATTAT	120
Qy	121	GGCAATTATCTTCCTCGTGGGATTTCCAGGCAATCAGTAGTGATATCCACTTACATTTTC	180
Db	121	GGCAATTATCTTCCTCGTGGGATTTCCAGGCAATCAGTAGTGATATCCACTTACATTTTC	180
Qy	181	AAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACTGGCTGCACAGATCTG	240
Db	181	AAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACTGGCTGCACAGATCTG	240

i ORGANISM: Human  
US-10-270-144-1

Query Match 99.8%; Score 1012.4; DB 14; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 1.6e-293;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATGAGCAGCCTAGACTATTTAGCAAAATCTTCTGATTTCCCGGATTTATGACAGTCTGCT	60
Db	1	ATGAATGAGCAGCCTAGACTATTTAGCAAAATCTTCTGATTTCCCGGATTTATGACAGTCTGCT	60
Qy	61	TTTGGAAATTCACCTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT	120
Db	61	TTTGGAAATTCACCTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT	120
Qy	121	GGCATTTCTTCCTCGTGGGATTTCCAGGCAATCGAGTAGTGATTCACCTTACATTTTC	180
Db	121	GGCATTTCTTCCTCGTGGGATTTCCAGGCAATCGAGTAGTGATTCACCTTACATTTTC	180
Qy	181	AAATGAGACCTTGGAGAGCAGCAGCACCATCAATTATGCTGAACCTGGCGTCGACAGATCTG	240
Db	181	AAATGAGACCTTGGAGAGCAGCAGCACCATCAATTATGCTGAACCTGGCGTCGACAGATCTG	240
Qy	241	CTGTATCTGACAGCCTCCCTTCTGATTCACCTACTATGCTAGTGGGGAACCTGGATC	300
Db	241	CTGTATCTGACAGCCTCCCTTCTGATTCACCTACTATGCTAGTGGGGAACCTGGATC	300
Qy	301	TTTGGAGATTCATGTTGAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
Db	301	TTTGGAGATTCATGTTGAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
Qy	361	ATCCTCTTCCTCAGCTGTTTCCAGCATCTCCGCTACTGTGATCAATTCACCCCAATGAGC	420
Db	361	ATCCTCTTCCTCAGCTGTTTCCAGCATCTCCGCTACTGTGATCAATTCACCCCAATGAGC	420
Qy	421	TGCTTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGTGCTGGTGTGGATCAAT	480
Db	421	TGCTTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGTGCTGGTGTGGATCAAT	480
Qy	481	TCATGTTAGTGTGAGTGTGATTCAGGATGACCTTCTTGATCAGATCAACCAAGAGGCAACAGA	540
Db	481	TCATGTTAGTGTGAGTGTGATTCAGGATGACCTTCTTGATCAGATCAACCAAGAGGCAACAGA	540
Qy	541	TCAGCTGTCTGACAGCCTCACCAGTTTCGGATGAACCTCAATATTAAGTGTGACACCTTA	600
Db	541	TCAGCTGTCTGACAGCCTCACCAGTTTCGGATGAACCTCAATATTAAGTGTGACACCTTA	600

Db 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAAATTAGTTACTCAACACACCTTGA 1014

RESULT 10

US-10-188-405-7  
Sequence 7, Application US/10188405  
Publication No. US20030082585A1

GENERAL INFORMATION:  
APPLICANT: Tian, Hui

APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long

APPLICANT: Zhao, Jiagang

APPLICANT: Cutler, Gene

APPLICANT: Tularik, Inc.

TITLE OF INVENTION: No. US20030082585A1el Receptors

FILE REFERENCE: 018781-008410US

CURRENT APPLICATION NUMBER: US/10/188,405

CURRENT FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: US 60/302,800

PRIOR FILING DATE: 2001-07-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 1014

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human TGR164

US-10-188-405-7

Query Match 99.8%; Score 1012.4; DB 14; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 1.6e-293;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATGAGCAGCCTAGACTATTTAGCAAAATCTTCTGATTTCCCGGATTTATGACAGTCTGCT	60
Db	1	ATGAATGAGCAGCCTAGACTATTTAGCAAAATCTTCTGATTTCCCGGATTTATGACAGTCTGCT	60
Qy	61	TTTGGAAATTCACCTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT	120
Db	61	TTTGGAAATTCACCTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT	120
Qy	121	GGCATTTCTTCCTCGTGGGATTTCCAGGCAATCGAGTAGTGATTCACCTTACATTTTC	180
Db	121	GGCATTTCTTCCTCGTGGGATTTCCAGGCAATCGAGTAGTGATTCACCTTACATTTTC	180
Qy	181	AAATGAGACCTTGGAGAGCAGCAGCACCATCAATTATGCTGAACCTGGCGTCGACAGATCTG	240
Db	181	AAATGAGACCTTGGAGAGCAGCAGCACCATCAATTATGCTGAACCTGGCGTCGACAGATCTG	240
Qy	241	CTGTATCTGACAGCCTCCCTTCTGATTCACCTACTATGCTAGTGGGGAACCTGGATC	300
Db	241	CTGTATCTGACAGCCTCCCTTCTGATTCACCTACTATGCTAGTGGGGAACCTGGATC	300
Qy	301	TTTGGAGATTCATGTTGAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
Db	301	TTTGGAGATTCATGTTGAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
Qy	361	ATCCTCTTCCTCAGCTGTTTCCAGCATCTCCGCTACTGTGATCAATTCACCCCAATGAGC	420
Db	361	ATCCTCTTCCTCAGCTGTTTCCAGCATCTCCGCTACTGTGATCAATTCACCCCAATGAGC	420
Qy	421	TGCTTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGTGCTGGTGTGGATCAAT	480
Db	421	TGCTTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGTGCTGGTGTGGATCAAT	480
Qy	481	TCATGTTAGTGTGAGTGTGATTCAGGATGACCTTCTTGATCAGATCAACCAAGAGGCAACAGA	540
Db	481	TCATGTTAGTGTGAGTGTGATTCAGGATGACCTTCTTGATCAGATCAACCAAGAGGCAACAGA	540
Qy	541	TCAGCTGTCTGACAGCCTCACCAGTTTCGGATGAACCTCAATATTAAGTGTGACACCTTA	600
Db	541	TCAGCTGTCTGACAGCCTCACCAGTTTCGGATGAACCTCAATATTAAGTGTGACACCTTA	600

QY 601 ATTGAGTCACTACTTTCTGCTCCCTCCCTGGTGTAGTGAACATTTGCTATACACG 660  
DB 601 ATTGAGTCACTACTTTCTGCTCCCTCCCTGGTGTAGTGAACATTTGCTATACACG 660  
QY 661 ATTATCCACACTCTGACCCATGAGTGAACATTTGAGTGTGCTTAAAGCAGAACGCA 720  
DB 661 ATTATCCACACTCTGACCCATGAGTGAACATTTGAGTGTGCTTAAAGCAGAACGCA 720  
QY 721 AGGTTAACCATTCTGCTACTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 780  
DB 721 AGGTTAACCATTCTGCTACTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 780  
QY 781 AGGTTAACCATTCTGCTACTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 840  
DB 781 AGGTTAACCATTCTGCTACTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 840  
QY 841 CATGAAGCTTACATCGTTTCTGAGCAACATTTGAGTGTGCTTCTGAGTGTGCTTCTG 900  
DB 841 CATGAAGCTTACATCGTTTCTGAGCAACATTTGAGTGTGCTTCTGAGTGTGCTTCTG 900  
QY 901 CATATGTGCTGTGCTGAGCAACATTTGAGTGTGCTTCTGAGTGTGCTTCTGAGTGT 960  
DB 901 CATATGTGCTGTGCTGAGCAACATTTGAGTGTGCTTCTGAGTGTGCTTCTGAGTGT 960  
QY 961 GTAAGCGGAACCTTTGAGCAACATTTGAGTGTGCTTCTGAGTGTGCTTCTGAGTGT 1014  
DB 961 GTAAGCGGAACCTTTGAGCAACATTTGAGTGTGCTTCTGAGTGTGCTTCTGAGTGT 1014

## RESULT 11

US-10-079-384-13  
; Sequence 13, Application US/10079384  
; Publication No. US20030108986A1  
; GENERAL INFORMATION:  
; APPLICANT: Communi, Didier  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 9409/2132  
; CURRENT APPLICATION NUMBER: US/10/079,384  
; CURRENT FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 09/885,453  
; PRIOR FILING DATE: 2001-06-20  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 1014  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1014)  
; OTHER INFORMATION:  
US-10-079-384-13

Query Match 99.8%; Score 1012.4; DB 15; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 1.6e-293;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATATGCACTGCT 60  
DB 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATATGCACTGCT 60  
QY 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
DB 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
QY 121 GCAATATCTTCTGCTGGGATTTCCAGCAATGCACTAGTGTATCCACTTACATTTTC 180  
DB 121 GCAATATCTTCTGCTGGGATTTCCAGCAATGCACTAGTGTATCCACTTACATTTTC 180  
QY 181 AAAATGAGACCTTGAAGAGCAGCAGCATTATGCTGAACTGGCTGCACTGCACTGCTG 240  
DB 181 AAAATGAGACCTTGAAGAGCAGCAGCATTATGCTGAACTGGCTGCACTGCACTGCTG 240

QY 241 CTGTATCTGACAGCCTCCCTTCTGATTCACTACTATGCGAGTGGCGAAACTGATC 300  
DB 241 CTGTATCTGACAGCCTCCCTTCTGATTCACTACTATGCGAGTGGCGAAACTGATC 300  
QY 301 TTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCCAGCTTCCATTTCAACCTGTATAGCAGC 360  
DB 301 TTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCCAGCTTCCATTTCAACCTGTATAGCAGC 360  
QY 361 ATCCCTTCTCCTCACTGTTTTCAGCATTTTCCGCTACTGTGTGATCATTTACCCAAATGAGC 420  
DB 361 ATCCCTTCTCCTCACTGTTTTCAGCATTTTCCGCTACTGTGTGATCATTTACCCAAATGAGC 420  
QY 421 TCGCTTTTCCATTCACAAAACCTCGATGTGCAAGTGTGAGCTGTGCTGTGTGGATCAIT 480  
DB 421 TCGCTTTTCCATTCACAAAACCTCGATGTGCAAGTGTGAGCTGTGCTGTGTGGATCAIT 480  
QY 481 TCACCTGGTAGCTGTCAATCCGATGACCTTTCTTGATCACAATCAACCAAGGACCAACAGA 540  
DB 481 TCACCTGGTAGCTGTCAATCCGATGACCTTTCTTGATCACAATCAACCAAGGACCAACAGA 540  
QY 541 TCAGCTGTCTCGACCTCACAGTTCCGATGAACCTCACTACTATTAAAGTGGTACACCTG 600  
DB 541 TCAGCTGTCTCGACCTCACAGTTCCGATGAACCTCACTACTATTAAAGTGGTACACCTG 600  
QY 601 ATTTTGACTGCAACTACTTTCTGCTCCCTCCCTTGGTGTAGTGTGACACTTTGCTATACACG 660  
DB 601 ATTTTGACTGCAACTACTTTCTGCTCCCTCCCTTGGTGTAGTGTGACACTTTGCTATACACG 660  
QY 661 ATTATCCACACTCTGACCCATGGAAGTGTGCAAACTGACAGCTGCTTAAAGCAGAACGCA 720  
DB 661 ATTATCCACACTCTGACCCATGGAAGTGTGCAAACTGACAGCTGCTTAAAGCAGAACGCA 720  
QY 721 AGGCTAAACATTTCTGCTACTCTCTGCAATTTACGATATGTTTTTACCCTTCCATATCTTG 780  
DB 721 AGGCTAAACATTTCTGCTACTCTCTGCAATTTACGATATGTTTTTACCCTTCCATATCTTG 780  
QY 781 AGGCTAAACATTTCTGCTACTCTCTGCAATTTACGATATGTTTTTACCCTTCCATATCTTG 840  
DB 781 AGGCTAAACATTTCTGCTACTCTCTGCAATTTACGATATGTTTTTACCCTTCCATATCTTG 840  
QY 841 CATGAAGCTTACATCGTTTCTGAGCAACATTTAGCTGTCTGAAACACCTTTGGTAACTGTTA 900  
DB 841 CATGAAGCTTACATCGTTTCTGAGCAACATTTAGCTGTCTGAAACACCTTTGGTAACTGTTA 900  
QY 901 CTATATGTGCTGTGCTGAGCAACATTTTCAGCAGGCTGTCTGCTCAACAGTGTAGATGCAAA 960  
DB 901 CTATATGTGCTGTGCTGAGCAACATTTTCAGCAGGCTGTCTGCTCAACAGTGTAGATGCAAA 960  
QY 961 GTAAGCGGAACCTTTGAGCAACATTTAGTGTACTCAACCAACCTTTGA 1014  
DB 961 GTAAGCGGAACCTTTGAGCAACATTTAGTGTACTCAACCAACCTTTGA 1014

## RESULT 12

US-10-225-567A-646  
; Sequence 646, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 646  
; LENGTH: 1014

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-646

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Query Match	99.8%	Score 1012.4	DB 15	Length 1014
Best Local Similarity	99.9%	Pred. No. 1.6e-293		
Matches 1013	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATATGACAGTGCT	60		
Db				
Qy 1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATATGACAGTGCT	60		
Db				
Qy 61	TTTGGAATATGCACTGATGAAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTAT	120		
Db				
Qy 61	TTTGGAATATGCACTGATGAAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTAT	120		
Db				
Qy 121	GGCAATATCTTCCCTGCGGGATTTCCAGGCAATGCGAGTAGTGATATCCACTTACATTTTC	180		
Db				
Qy 121	GGCAATATCTTCCCTGCGGGATTTCCAGGCAATGCGAGTAGTGATATCCACTTACATTTTC	180		
Db				
Qy 181	AAAATGAGACTTGGAGAGCAGACAATATATGCTGAAACCTGGCCCTGCACAGATCTG	240		
Db				
Qy 181	AAAATGAGACTTGGAGAGCAGACAATATATGCTGAAACCTGGCCCTGCACAGATCTG	240		
Db				
Qy 241	CTGTATCTGACAGCCTCCCTCTCTGATTCACCTACTATGCGAGTGGGGAACCTGGATC	300		
Db				
Qy 241	CTGTATCTGACAGCCTCCCTCTCTGATTCACCTACTATGCGAGTGGGGAACCTGGATC	300		
Db				
Qy 301	TTTGGAGATTTCACTGTGAAGTTTATCCGCTTCAGCTTCCATTTCAAACCTGATAGCAGC	360		
Db				
Qy 301	TTTGGAGATTTCACTGTGAAGTTTATCCGCTTCAGCTTCCATTTCAAACCTGATAGCAGC	360		
Db				
Qy 361	ATCCTCTTCCTCACCTGTTTCAGCATCTTCGGCTACTGTGTGATCAITTCACCAATGAGC	420		
Db				
Qy 361	ATCCTCTTCCTCACCTGTTTCAGCATCTTCGGCTACTGTGTGATCAITTCACCAATGAGC	420		
Db				
Qy 421	TGCTTTTCCATTCACAAACTCGATGCGAGTTGTAGCCTGTGCTGTGGTGTGGATCAIT	480		
Db				
Qy 421	TGCTTTTCCATTCACAAACTCGATGCGAGTTGTAGCCTGTGCTGTGGTGTGGATCAIT	480		
Db				
Qy 481	TCAGTGTGAGTGTCTCATTCGGATGACCTTTCTTGATCAGATCAACCAACAGGACCAACAGA	540		
Db				
Qy 481	TCAGTGTGAGTGTCTCATTCGGATGACCTTTCTTGATCAGATCAACCAACAGGACCAACAGA	540		
Db				
Qy 541	TCAGCCTGTCTCGACCTCACAGTTCGAGTGAATCAATACTATTAAGTGGTACAACTTA	600		
Db				
Qy 541	TCAGCCTGTCTCGACCTCACAGTTCGAGTGAATCAATACTATTAAGTGGTACAACTTA	600		
Db				
Qy 601	ATTTTGACTGCAACTACTTTTCTGCTCCCTTGGTGATGACACTTTGCTATACCAAG	660		
Db				
Qy 601	ATTTTGACTGCAACTACTTTTCTGCTCCCTTGGTGATGACACTTTGCTATACCAAG	660		
Db				
Qy 661	ATTATCCACACTCTGACCCATGGAATGCAAACTGACAGCTGCTTTAAGCAGAAAGACAGA	720		
Db				
Qy 661	ATTATCCACACTCTGACCCATGGAATGCAAACTGACAGCTGCTTTAAGCAGAAAGACAGA	720		
Db				
Qy 721	AGGCTAACCAATCTGCTACTCTCTGCAATTTTACGTATGTTTTTACCTTCCATATCTTG	780		
Db				
Qy 721	AGGCTAACCAATCTGCTACTCTCTGCAATTTTACGTATGTTTTTACCTTCCATATCTTG	780		
Db				
Qy 781	AGGGTCATTTCGGATCGGAATCTCGCTCTTCCAAATCAGTTGTTCCATTCAGAGATCAGATC	840		
Db				
Qy 781	AGGGTCATTTCGGATCGGAATCTCGCTCTTCCAAATCAGTTGTTCCATTCAGAGATCAGATC	840		
Db				
Qy 841	CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTTGAAACCTTTTGGTAACCTGTTA	900		
Db				
Qy 841	CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTTGAAACCTTTTGGTAACCTGTTA	900		
Db				
Qy 901	CTATATGTGGTGTGAGCAGACACTTTCAGCAGGCTGTCTGCTTCACACTGTGAGATGCBA	960		
Db				
Qy 901	CTATATGTGGTGTGAGCAGACACTTTCAGCAGGCTGTCTGCTTCACACTGTGAGATGCBA	960		
Db				
Qy 961	GTAAAGCGGAAACCTTTCAGCAGCAAGCAAGAAAAATAGTTACTTCAAAACCAACCTTGA	1014		
Db				

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RESULT 13
US-10-321-807-27
; Sequence 27, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong T.
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-E
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCY/US99/29398
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-27

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Query Match	99.8%;	Score 1012.4;	DB 15;	Length 1014;
Best Local Similarity	99.9%;	Pred. No. 1.6e-293;		
Matches 1013;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCGATTTCCCGGATTTATGCAGCTGCT	60	
DB	1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCGATTTCCCGGATTTATGCAGCTGCT	60	
QY	61	TTTCGAAATTCACCTGATGAAACACATCCCACTCAAGATGCACCTCCCTGTTATTATTAT	120	
DB	61	TTTCGAAATTCACCTGATGAAACATCCCACTCAAGATGCACCTCCCTGTTATTATTAT	120	
QY	121	GGCATTATCTTCCTCGTGGGATTTCCAGGCAATCCAGTAGTGATATCCACTTACATTTTC	180	
DB	121	GGCATTATCTTCCTCGTGGGATTTCCAGGCAATCCAGTAGTGATATCCACTTACATTTTC	180	
QY	181	AAATGAGACCTTGGAGAGCAGCACCATCATATGCTGAACTGGCGTGCACAGACTG	240	
DB	181	AAATGAGACCTTGGAGAGCAGCACCATCATATGCTGAACTGGCGTGCACAGACTG	240	
QY	241	CTGTATCTGACAGCCTCCCTCTCTGATTCACCTACTATGCGAGTGGCGAAACTGGATC	300	
DB	241	CTGTATCTGACAGCCTCCCTCTCTGATTCACCTACTATGCGAGTGGCGAAACTGGATC	300	
QY	301	TTTGGAGATTTCACTGTGAAGTTTATCCGTTTCAGCTTCCAATTTCAACCTGTATAGCAGC	360	
DB	301	TTTGGAGATTTCACTGTGAAGTTTATCCGTTTCAGCTTCCAATTTCAACCTGTATAGCAGC	360	



Qy	361	ATCCTCTTCCTCA	CTGTTTTCAGCAATCTTCGCTACTGTTGATCA	TCATTCACCAATGAGC	420
Db	361	ATCCTCTTCCTCA	CTGTTTTCAGCAATCTTCGCTACTGTTGATCA	TCATTCACCAATGAGC	420
Qy	421	TGCTTTTCCATTC	CAAAACCTCGATGTCAGTTGTAGCCTGCTGCTGGTGGTGGATCA	TT	480
Db	421	TGCTTTTCCATTC	CAAAACCTCGATGTCAGTTGTAGCCTGCTGCTGGTGGTGGATCA	TT	480
Qy	481	TCACTGGTAGTG	TCAATTCGCGATGACCTTCTTGATCA	CAATCAACCAACAGGACCAACAGA	540
Db	481	TCACTGGTAGTG	TCAATTCGCGATGACCTTCTTGATCA	CAATCAACCAACAGGACCAACAGA	540
Qy	541	TCAGCTGTCTCG	ACCTCACCAGTTCGGATGAACTCAATACTATTA	TAAAGTGGTAAACCTTA	600
Db	541	TCAGCTGTCTCG	ACCTCACCAGTTCGGATGAACTCAATACTATTA	TAAAGTGGTAAACCTTA	600
Qy	601	ATTTTGACTGCA	ACTATTTCTGCTCCCTTGGTGATGTAGACACTTTTGCTATACCA	CAG	660
Db	601	ATTTTGACTGCA	ACTATTTCTGCTCCCTTGGTGATGTAGACACTTTTGCTATACCA	CAG	660
Qy	661	ATTATCCACACT	CTGACCCATGGACTGCAAACTGACAGCTGCCTTA	AAGCAGAAACAGCA	720
Db	661	ATTATCCACACT	CTGACCCATGGACTGCAAACTGACAGCTGCCTTA	AAGCAGAAACAGCA	720
Qy	721	AGGCTAAACCA	TTCTGTACTCTTTGCAATTTTACGTATGTTTTTACCCCTCCCATATCT	TTG	780
Db	721	AGGCTAAACCA	TTCTGTACTCTTTGCAATTTTACGTATGTTTTTACCCCTCCCATATCT	TTG	780
Qy	781	AGGCTCAATCG	GATCGGAATCTCGCTGCTTTCAATCAATCAATGTTTCCATTTGAGAATCAGATC		840
Db	781	AGGCTCAATCG	GATCGGAATCTCGCTGCTTTCAATCAATCAATGTTTCCATTTGAGAATCAGATC		840
Qy	841	CATGAAGCTTAC	ATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAA	CTGTTTA	900
Db	841	CATGAAGCTTAC	ATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAA	CTGTTTA	900
Qy	901	CTATATGTGGT	GTGTCAGCGAACTTTTCAGCAGGCTGTCTCTCAACAGTCAGATGCAAA		960
Db	901	CTATATGTGGT	GTGTCAGCGAACTTTTCAGCAGGCTGTCTCTCAACAGTCAGATGCAAA		960
Qy	961	GTAAAGCGGGA	ACCTTTAGACGAAGCAAGAAATTAAGTTACTCAAA	CAACCCCTTGA	1014
Db	961	GTAAAGCGGGA	ACCTTTAGACGAAGCAAGAAATTAAGTTACTCAAA	CAACCCCTTGA	1014

QY	61	TTTGGAAATTGCACTGATGAAACATCCCACTCAAGATGCACCTACCTCCCTGTTATTTAT	120
DB	61	TTTTGGAAATTGCACTGATGAAACATCCCACTCAAGATGCACCTACCTCCCTGTTATTTAT	120
QY	121	GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCACTTACATTTTC	180
DB	121	GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCACTTACATTTTC	180
QY	181	AAAATGAGACCTTGGAAAGAGCAGACCACTCATTTAGCTGAACTGGCTGCACAGATCTG	240
DB	181	AAAATGAGACCTTGGAAAGAGCAGACCACTCATTTAGCTGAACTGGCTGCACAGATCTG	240
QY	241	CTGTATCTGACAGGCTCCCTTCCTGATTCACATCTATGTCGAACCTGGCCCTGCACAGATCTG	300
DB	241	CTGTATCTGACAGGCTCCCTTCCTGATTCACATCTATGTCGAACCTGGCCCTGCACAGATCTG	300
QY	301	TTTGGAGATTTCAATGTGTAAAGTTTATCCGCTTCAGCTTCCATTTTCAACCTGTATAGCAGC	360
DB	301	TTTGGAGATTTCAATGTGTAAAGTTTATCCGCTTCAGCTTCCATTTTCAACCTGTATAGCAGC	360
QY	361	ATCCTCTTCTCACCTGTTTCAGCATCTTCGGCTACTGTGTGATCATTTCAACCCTGATAGCAGC	420
DB	361	ATCCTCTTCTCACCTGTTTCAGCATCTTCGGCTACTGTGTGATCATTTCAACCCTGATAGCAGC	420
QY	421	TGCTTTTCCATTACAAAACTCGATGTGCGAGTTGTAGCCTGTGCTGGTGTGGATCAATT	480
DB	421	TGCTTTTCCATTACAAAACTCGATGTGCGAGTTGTAGCCTGTGCTGGTGTGGATCAATT	480
QY	481	TCACTGTGTAGCTGTCATTTCGGATGACCTCTTGATCACATCAACCAACAGGACCAACAGA	540
DB	481	TCACTGTGTAGCTGTCATTTCGGATGACCTCTTGATCACATCAACCAACAGGACCAACAGA	540
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DB	541	TCAGCCTGTCTCGACCTCACCAGTTCCGATGCAACTCAATACTATTAAGTGGTACAACCTG	600
QY	601	ATTTTGACTGCAACTACTTTCTGCTCCCTTCGGTGATGTGACATTTTCTATACCAAG	660
DB	601	ATTTTGACTGCAACTACTTTCTGCTCCCTTCGGTGATGTGACATTTTCTATACCAAG	660
QY	661	ATTATCCACACTTGACCCATGAGCTGCAACCTGACAGCTGCCTTAGCAGGAAGACAGA	720
DB	661	ATTATCCACACTTGACCCATGAGCTGCAACCTGACAGCTGCCTTAGCAGGAAGACAGA	720
QY	721	AGGCTAACCAATCTGCTACTCTTCGATTTTADGATATGTTTTTACCCCTTCCAATCTCTG	780
DB	721	AGGCTAACCAATCTGCTACTCTTCGATTTTADGATATGTTTTTACCCCTTCCAATCTCTG	780
QY	781	AGGGTCATTCCGGATCGAATCTCGCTGCTTTCAATCAAGTGTTCCTATGAGAAATCAGATC	840
DB	781	AGGGTCATTCCGGATCGAATCTCGCTGCTTTCAATCAAGTGTTCCTATGAGAAATCAGATC	840
QY	841	CATGAAGCTTACATCGTTTTCTAGACCAATAGCTGCTCTGAAACACCTTTGGTAACCTGTTA	900
DB	841	CATGAAGCTTACATCGTTTTCTAGACCAATAGCTGCTCTGAAACACCTTTGGTAACCTGTTA	900
QY	901	CTATATGTGTGTGACGCAAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA	960
DB	901	CTATATGTGTGTGACGCAAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA	960
QY	961	GTAAGCGGNAACCTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTGA	1014
DB	961	GTAAGCGGNAACCTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTGA	1014

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Query Match      99.8%; Score 1012.4; DB 16; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATATGACAGTGT 60
db 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATATGACAGTGT 60

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; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343.650A
; PRIOR FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-10-343-650A-13

Query Match      99.8%; Score 1012.4; DB 16; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTATGCGAGCTGCT 60
Db      1  ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTATGCGAGCTGCT 60

Qy      61  TTTGGAAATTCGACTGATGAACATCCCACTCAAGATGCACACTACCTCCCTGTTATTAT 120
Db      61  TTTGGAAATTCGACTGATGAACATCCCACTCAAGATGCACACTACCTCCCTGTTATTAT 120

Qy      121  GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTGAATCCACTTACATTTTC 180
Db      121  GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTGAATCCACTTACATTTTC 180

Qy      181  AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCCTGCACAGATCTG 240
Db      181  AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCCTGCACAGATCTG 240

Qy      241  CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCCAGTGGCGAAACCTGGATC 300
Db      241  CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCCAGTGGCGAAACCTGGATC 300

Qy      301  TTTGGAGATTTTCATGTTAAAGTTTATCCGCTTCAGCTTCCATTTCAAACCTGTATAGCAGC 360
Db      301  TTTGGAGATTTTCATGTTAAAGTTTATCCGCTTCAGCTTCCATTTCAAACCTGTATAGCAGC 360

Qy      361  ATCCCTCTTCTCACCCTGTTTCAGCATCTTCCGCTACTGTGATCATTCACCCCAATGAGC 420
Db      361  ATCCCTCTTCTCACCCTGTTTCAGCATCTTCCGCTACTGTGATCATTCACCCCAATGAGC 420

Qy      421  TGCTTTTCCATTCAAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGCTGTGGTGGATCATT 480
Db      421  TGCTTTTCCATTCAAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGCTGTGGTGGATCATT 480

Qy      481  TCACCTGGTAGCTGTGATTCGGATGACCTTCTTGTATCACAATCAACCAAGGACCAACAGA 540
Db      481  TCACCTGGTAGCTGTGATTCGGATGACCTTCTTGTATCACAATCAACCAAGGACCAACAGA 540

Qy      541  TCAGCTGTCTCGACCTCAACCTACCGATTCGGATGAACCTCAATACCTATTAAAGTGGTACACCTA 600
Db      541  TCAGCTGTCTCGACCTCAACCTACCGATTCGGATGAACCTCAATACCTATTAAAGTGGTACACCTG 600

Qy      601  ATTTTGGACTGCACTACTTTCTGCTCCCTTGGTATGATGACACTTTGCTATACCAG 660
Db      601  ATTTTGGACTGCACTACTTTCTGCTCCCTTGGTATGATGACACTTTGCTATACCAG 660

Qy      661  ATTATCCACACTCTGACCCCTAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCACGA 720
Db      661  ATTATCCACACTCTGACCCCTAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCACGA 720

Qy      721  AGGCTAAACATCTCTGCTACTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780
Db      721  AGGCTAAACATCTCTGCTACTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780
```

Search completed: November 1, 2004, 21:46:06  
Job time : 567 secs

```
Qy      781  AGGTCATTCGGATCGAATCTCGCTGCTTTCAATCAAGTTGTTCCATTGGAATCAGATC 840
Db      781  AGGTCATTCGGATCGAATCTCGCTGCTTTCAATCAAGTTGTTCCATTGGAATCAGATC 840

Qy      841  CATGAAGCTTACATCGTTTCTAGACCAATTAGCTGCTGGAACACCTTTGGTAACCTGTTA 900
Db      841  CATGAAGCTTACATCGTTTCTAGACCAATTAGCTGCTGGAACACCTTTGGTAACCTGTTA 900

Qy      901  CTATATGTGTGCTGAGCGACAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACAACCCCTTGA 960
Db      901  CTATATGTGTGCTGAGCGACAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACAACCCCTTGA 960

Qy      961  GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACAACCCCTTGA 1014
Db      961  GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTAAGTTACTCAAAACAACCCCTTGA 1014
```

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1014	100.0	1014	6	AAd26370	Human G-p
2	1014	100.0	1014	6	AAAD34278	Human AXO
3	1014	100.0	1014	6	ABQ78847	Human G-p
4	1014	100.0	1014	6	ABQ51730	Human nov
5	1014	100.0	1851	6	ABSS1678	Human encod
6	1012.4	99.8	1014	5	AA507948	Human CDN
7	1012.4	99.8	1014	6	ABN85630	Human P2Y
8	1012.4	99.8	1014	6	AAK98323	Human pur
9	1012.4	99.8	1014	6	ABK11381	Human DNA
10	1012.4	99.8	1014	6	ABE242876	Human GPC
11	1012.4	99.8	1014	8	ABE59170	Human TGR
12	1012.4	99.8	1014	8	ABE242582	Human G p
13	1012.4	99.8	1014	10	ADCC25997	Human pur
14	1012.4	99.8	1014	10	ADAE61652	Human GPC
15	1012.4	99.8	1014	11	ADL96473	Human G p
16	1012.4	99.8	1014	12	ADM10573	Human G p
17	1012.4	99.8	1014	12	ADQ23940	Human P2Y
18	1012.4	99.8	1029	8	ADQ50885	Human GPC
19	1012.4	99.8	1081	6	ABSS59232	TARZAN DN
20	1012.4	99.8	1081	6	ABSS50883	Human G-p
21	1012.4	99.8	1288	8	ABL561197	Human TAR

## ALIGNMENTS

## RESULT 1

AAD26370

ID AAD2

XX

AC AAD2

XX

DT 26-M

XX DE

DE  
yy  
HumaXX  
KW  
HumaKW  
arter  
HumeKW Alzh  
KW Alzh

KW athe

KW gast

KW acqu

KW Addi  
KW Addi

KW  
YY  
diab

SO  
YY  
HomcXX  
XX  
XXXXX

**Key**

FT CDS

LE

LE

XX  
NDPN  
WO20  
XX

22-N-

XX  
XX

PF 17-M

XX

PR 18-M

PR 22-M  
DD 25-M

PR 25-M  
PR 02-T

PR 02-J  
PR 02-JXX  
02-0

PA (INC

XX

PI  
Patt

PI Khan

Ellis

XX

DR WPI: 2002-089844/12.  
DR P-PSDB; AAE16171.  
XX Novel G-protein coupled receptors and polynucleotides useful for  
PT diagnosis, treatment and prevention of disorders of cell proliferation,  
PT neurological, cardiovascular, metabolic disorders and viral infections.  
XX Claim 5; Page 111-112; 115pp; English.  
XX The invention relates to human G-protein coupled receptor (GPCR)  
CC polypeptides and polynucleotides. GPCR polypeptides are useful for  
CC screening compounds that modulate their activity. They are useful in the  
CC diagnosis, prevention and treatment of disorders which include cell  
CC proliferative disorders such as arteriosclerosis, hepatitis,  
CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,  
CC lymphoma; neurological disorders such as epilepsy, ischaemic  
CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,  
CC Parkinson's disease, ataxia, multiple sclerosis, bacterial and viral  
CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;  
CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,  
CC hypertension, vascular tumours, myocardial infarction, hypertensive heart  
CC disease, infective endocarditis, cardiomyopathy, myocarditis;  
CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,  
CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,  
CC constipation, acquired immune deficiency syndrome (AIDS), hepatic  
CC encephalopathy; autoimmune/inflammatory disorders such as Addison's  
CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact  
CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,  
CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid  
CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,  
CC fungal, parasitic, protozoal and helminthic infections and trauma;  
CC metabolic disorders such as diabetes, obesity and osteoporosis; and viral  
CC infections such as infection caused by viral agent classified as  
CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are  
CC useful as probes for assessing toxicity of test compounds. They are also  
CC used in gene therapy. The present sequence is human G-protein coupled  
CC receptor 2 (GPCR-2) cDNA  
XX Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1014; DB 6; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 1.9e-289;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATGAGCCACTAGACTATTTAGCAATGCTCTGATTTCCCGATATGACGTGCT 60  
DB 1 ATGAATGAGCCACTAGACTATTTAGCAATGCTCTGATTTCCCGATATGACGTGCT 60  
QY 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGACCTACCTCCCTGTTATTTAT 120  
DB 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGACCTACCTCCCTGTTATTTAT 120  
QY 121 GGCATTATCTCTCTGCGGATTTCCAGGAATGCGAGTAGTGATATCCACTTACATTTTC 180  
DB 121 GGCATTATCTCTCTGCGGATTTCCAGGAATGCGAGTAGTGATATCCACTTACATTTTC 180  
QY 181 AAAATGAGACTTGGAGAGACAGACCAATCATTTATGCTGAACTGCGCTGCACAGATCTG 240  
DB 181 AAAATGAGACTTGGAGAGACAGACCAATCATTTATGCTGAACTGCGCTGCACAGATCTG 240  
QY 241 CTGTATCTGACAGCCCTCCCTCTCTGATTCATCTATGCTGCGGAAACTGGATC 300  
DB 241 CTGTATCTGACAGCCCTCCCTCTCTGATTCATCTATGCTGCGGAAACTGGATC 300  
QY 301 TTGGAGATTTCATGTTAGTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
DB 301 TTGGAGATTTCATGTTAGTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
QY 361 ATCCTCTCTCAGCTGTTTCAGCATCTCGGCTACTGCTGATTCATTCACCAATGAGC 420  
DB 361 ATCCTCTCTCAGCTGTTTCAGCATCTCGGCTACTGCTGATTCATTCACCAATGAGC 420  
QY 421 TGCTTTTCCATTCAAAACCTCGATGTCAGTTGTAGCCTGTGCTGTGGATCATTT 480

Db 421 TGCTTTTCCATTCAAAACCTCGATGTCAGTTGTAGCCTGTGCTGTGGATCATTT 480  
QY 481 TCACCTGTAGTGCTGATTCGATGACCTTCTTGATCACATCAACCAACAGACCAACAGA 540  
Db 481 TCACCTGTAGTGCTGATTCGATGACCTTCTTGATCACATCAACCAACAGACCAACAGA 540  
QY 541 TCAGCCTGTCTCGACCTCACAGTTCGATGAACTCAATATCTATTAAGTGTGATACCTA 600  
Db 541 TCAGCCTGTCTCGACCTCACAGTTCGATGAACTCAATATCTATTAAGTGTGATACCTA 600  
QY 601 ATTTTGTAGTCAACTTCTTCTGCTCCCTGTTGATGACACTTTTGTATACCAACG 660  
Db 601 ATTTTGTAGTCAACTTCTTCTGCTCCCTGTTGATGACACTTTTGTATACCAACG 660  
QY 661 ATTTTGTAGTCAACTTCTTCTGCTCCCTGTTGATGACACTTTTGTATACCAACG 660  
Db 661 ATTTTGTAGTCAACTTCTTCTGCTCCCTGTTGATGACACTTTTGTATACCAACG 660  
QY 720 ATTTTGTAGTCAACTTCTTCTGCTCCCTGTTGATGACACTTTTGTATACCAACG 720  
Db 720 ATTTTGTAGTCAACTTCTTCTGCTCCCTGTTGATGACACTTTTGTATACCAACG 720  
QY 780 AGGCTAACCAATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCCATATCTTG 780  
Db 780 AGGCTAACCAATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCCATATCTTG 780  
QY 840 AGGCTAACCAATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCCATATCTTG 840  
Db 840 AGGCTAACCAATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCCATATCTTG 840  
QY 900 CATGAAGCTTATCATCTGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
Db 900 CATGAAGCTTATCATCTGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
QY 960 CTATATGTTGTTGTCAGCGCAACCTTTTTCAGAGGCTGCTGCTCAACAGTGTAGTGCAA 960  
Db 960 CTATATGTTGTTGTCAGCGCAACCTTTTTCAGAGGCTGCTGCTCAACAGTGTAGTGCAA 960  
QY 961 GTAAGCGGAACTTTGAGCAAGCAAGAAATAGTTACTCAACCAACCTTTGA 1014  
Db 961 GTAAGCGGAACTTTGAGCAAGCAAGAAATAGTTACTCAACCAACCTTTGA 1014

RESULT 2  
AAD34278  
ID AAD34278 standard; cDNA; 1014 BP.  
XX  
AC AAD34278;  
DT 16-JUL-2002 (first entry)  
XX  
DE Human AXOR89 (G-protein coupled receptor) cDNA.  
XX  
KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;  
KW infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;  
KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;  
KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;  
KW myocardial infarction; allergy; benign prostatic hyperplasia; migraine;  
KW vomiting; psychotic; neurological disorder; anxiety; manic depression;  
KW delirium; Huntington's Disease; Gilles de la Tourette's syndrome;  
KW dementia; dyskinesia; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1. 1014  
FT /\*tag= a  
FT /product= "Human AXOR89 protein"  
XX  
PN GB2365012-A.  
XX  
PD 13-FEB-2002.  
XX  
PF 10-MAY-2001; 2001GB-00011437.  
XX  
PR 11-MAY-2000; 2000US-00569137.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX Elshourbagy N, Shabon U;  
XX WPI; 2002-332558/37.  
DR P-PSDB; AAE21803.  
XX Novel AXOR89 polypeptide and polynucleotide encoding it, useful for  
PT identifying agonists and antagonists in the treatment of diseases  
PT associated with an AXOR89 imbalance, such as cancers, diabetes or asthma.  
XX  
PS Claim 2; Page 30; 37pp; English.  
XX  
CC The invention relates to an isolated AXOR89 polypeptide (G-protein  
CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide  
CC and polynucleotide encoding the polypeptide, is useful for identifying  
CC agonists and antagonists (or inhibitors) that are potentially useful in  
CC treating conditions associated with an AXOR89 imbalance, such as  
CC bacterial, fungal or protozoan infections, cancers, pain, asthma,  
CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart  
CC failure, hypotension, hypertension, urinary retention, osteoporosis,  
CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign  
CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological  
CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,  
CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's  
CC syndrome. The polynucleotide sequence may also be used for chromosome  
CC localisation or tissue expression studies. The AXOR89 is used as a  
CC vaccine or to produce fusion proteins. The present sequence is human  
CC AXOR89 cDNA  
XX  
SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 6; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 1.9e-289;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60  
Db 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60  
QY 61 TTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120  
Db 61 TTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120  
QY 121 GCATTATCTCTCTGCGGATTTCCAGCAATGCACTAGTAGTATCCACTTACATTTTC 180  
Db 121 GCATTATCTCTCTGCGGATTTCCAGCAATGCACTAGTAGTATCCACTTACATTTTC 180  
QY 181 AAAATGAGACCTTTGGAAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240  
Db 181 AAAATGAGACCTTTGGAAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240  
QY 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTACTGTCAGTGGCGAAACCTGGATC 300  
Db 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTACTGTCAGTGGCGAAACCTGGATC 300  
QY 301 TTTGGAGATTTCACTGTAAGTTATCCGCTTACCTTCAGCTTCATTTCAACCTGTATAGCAGC 360  
Db 301 TTTGGAGATTTCACTGTAAGTTATCCGCTTACCTTCAGCTTCATTTCAACCTGTATAGCAGC 360  
QY 361 ATCCCTTCTCTCCTCAGCTTTTCCAGATCTTCCGCTTACCTGTATGATCATTCACCCCAATGAGC 420  
Db 361 ATCCCTTCTCTCCTCAGCTTTTCCAGATCTTCCGCTTACCTGTATGATCATTCACCCCAATGAGC 420  
QY 421 TGCTTTTCCATTCAAAAACTCGATGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 480  
Db 421 TGCTTTTCCATTCAAAAACTCGATGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 480  
QY 481 TCACCTGGTAGCTGTCTATCCGATGACCTTTCTTGATCACAATCAACCAAGGACCAACAGA 540  
Db 481 TCACCTGGTAGCTGTCTATCCGATGACCTTTCTTGATCACAATCAACCAAGGACCAACAGA 540

QY 541 TCAGCCTGTCTCGACCTCACCAGTTCCGATGAACCTCAATTAAGTGGTACACCTA 600  
Db 541 TCAGCCTGTCTCGACCTCACCAGTTCCGATGAACCTCAATTAAGTGGTACACCTA 600  
QY 601 ATTTTGACTGCAACTACTTTCTGCCTCCCTTGGTATGATGACACTTTGCTATACCACG 660  
Db 601 ATTTTGACTGCAACTACTTTCTGCCTCCCTTGGTATGATGACACTTTGCTATACCACG 660  
QY 661 ATTATCCACACTCTGACCCATGCAAACTGCAAGCTGCCTTAAGCAGAAAGCAGCA 720  
Db 661 ATTATCCACACTCTGACCCATGCAAACTGCAAGCTGCCTTAAGCAGAAAGCAGCA 720  
QY 721 AGGCTAACCACTCTGCTACTCTCTTGCATTTTACGTATGTTTACCCITCCATATCTTG 780  
Db 721 AGGCTAACCACTCTGCTACTCTCTTGCATTTTACGTATGTTTACCCITCCATATCTTG 780  
QY 781 AGGCTCATTTGGGATCGAATCTCCGCTGCTTCAATCAGTTGTTCCATTGAGAATCAGATC 840  
Db 781 AGGCTCATTTGGGATCGAATCTCCGCTGCTTCAATCAGTTGTTCCATTGAGAATCAGATC 840  
QY 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
Db 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
QY 901 CTATATGTGTGTGTCAGCAGCACTTTTCAGCAGGCTGCTGCTCAACAGTGAATGCAAA 960  
Db 901 CTATATGTGTGTGTCAGCAGCACTTTTCAGCAGGCTGCTGCTCAACAGTGAATGCAAA 960  
QY 961 GTAAGCGGGAACCTTGAGCAAGCAAAAGAAATTAGTTACTCAAAACACCTTGA 1014  
Db 961 GTAAGCGGGAACCTTGAGCAAGCAAAAGAAATTAGTTACTCAAAACACCTTGA 1014

RESULT 3  
ABQ78847  
ID ABQ78847 standard; cDNA; 1014 BP.  
XX  
AC ABQ78847;  
XX  
DT 04-OCT-2002 (first entry)  
XX  
DE Human G-protein coupled receptor PFI-019 cDNA.  
XX  
KW Human: G-protein coupled receptor; GPCR; PFI-019; neuroprotective;  
KW anti-inflammatory; cyostatic; cardiovascular; antiallergic; hypotensive;  
KW antiarteriosclerotic; osteopathic; hypertension; asthma;  
KW artherosclerosis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1014  
FT /\*tag= a  
FT /product= "PFI-019"  
XX  
PN EP1219638-A2.  
XX  
PD 03-JUL-2002.  
XX  
PF 04-DEC-2001; 2001EP-00310136.  
XX  
PR 18-DEC-2000; 2000GB-00030854.  
XX 04-MAY-2001; 2001GB-00011031.  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX Fidock MD;  
XX WPI; 2002-521945/56.  
DR P-PSDB; ABB81902.  
XX

PT New G-protein coupled receptor (GPCR) polypeptide with homology to p2Y  
PT purinoreceptor, useful for treating e.g. inflammation or cancers in a  
PT patient, or for screening GPCR agonists or antagonists for treating these  
PT diseases.

XX Claim 1; Page 12; 19pp; English.

XX The invention relates to a novel G-protein coupled receptor (GPCR), and  
CC the polynucleotide encoding it. The protein of the invention has  
CC neuroprotective, anti-inflammatory, cytoskeletal, cardiovascular,  
CC antiallergic, hypotensive, antiarteriosclerotic, and osteoprotective  
CC activity. The GPCR polypeptide is useful for manufacturing a medicament  
CC for treating a patient who needs to upregulate a receptor. Preferably,  
CC therapeutically useful areas are hypertension, asthma, and  
CC arteriosclerosis. The sequence encodes the G-protein coupled receptor of  
CC the invention, pfr-019

XX SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 6; Length 1014;

Best Local Similarity 100.0%; Pred. No. 1.9e-289; Indels 0; Gaps 0;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTATGCGTGTCT	60
DB	1	ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTATGCGTGTCT	60
QY	61	TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTTAT	120
DB	61	TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTTAT	120
QY	121	GCATATATCTTCTGCGGATTTCCAGCAATGAGTAGTATGATATCCACTTACATTTTC	180
DB	121	GCATATATCTTCTGCGGATTTCCAGCAATGAGTAGTATGATATCCACTTACATTTTC	180
QY	181	AAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCCTGCACAGATCTG	240
DB	181	AAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCCTGCACAGATCTG	240
QY	241	CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGGAAACTGGATC	300
DB	241	CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGGAAACTGGATC	300
QY	301	TTTGGAGATTGATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
DB	301	TTTGGAGATTGATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
QY	361	ATCCTCTTCTCCTCAGCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTCACCAATGAGC	420
DB	361	ATCCTCTTCTCCTCAGCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTCACCAATGAGC	420
QY	421	TGCTTTTCCATTCACAAAACCTGATGCGATGCTGAGCTGCTGCTGTGGTGGATCATTT	480
DB	421	TGCTTTTCCATTCACAAAACCTGATGCGATGCTGAGCTGCTGCTGTGGTGGATCATTT	480
QY	481	TCAGTGTAGCTCTCATTCGATGACCTTCTGATCACAATCAACAGCAGCAACACAGA	540
DB	481	TCAGTGTAGCTCTCATTCGATGACCTTCTGATCACAATCAACAGCAGCAACACAGA	540
QY	541	TCAGCTGTCTGACCTTCCAGCTTCCGATGAACTCAATCACTATTAAAGTGGTACACCTA	600
DB	541	TCAGCTGTCTGACCTTCCAGCTTCCGATGAACTCAATCACTATTAAAGTGGTACACCTA	600
QY	601	ATTTGACGTGCACTACTTTCTGCTCCCTTGGTGTAGTGTGACACTTTGCTATACACG	660
DB	601	ATTTGACGTGCACTACTTTCTGCTCCCTTGGTGTAGTGTGACACTTTGCTATACACG	660
QY	661	ATTATCCACTCTGACCCCTGAGCTGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGCA	720
DB	661	ATTATCCACTCTGACCCCTGAGCTGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGCA	720
QY	721	AGGCTAACCAATCTGCTACTCTTCAATTTTACGTATGTTTTTACCCCTTCCATATCTTG	780

DB	721	AGGCTAACCAATCTGCTACTCTTGCATTTTACGTATGTTTTTACCCCTTCCATATCTTG	780
QY	781	AGGCTAACCAATCTGCTACTCTTGCATTTTACGTATGTTTTTACCCCTTCCATATCTTG	840
DB	781	AGGCTAACCAATCTGCTACTCTTGCATTTTACGTATGTTTTTACCCCTTCCATATCTTG	840
QY	841	CATGAAGCTTACATCTGTTTCTAGACCAATAGCTGCTCTGAAACAACCTTGGTAACTGTTA	900
DB	841	CATGAAGCTTACATCTGTTTCTAGACCAATAGCTGCTCTGAAACAACCTTGGTAACTGTTA	900
QY	901	CTATATGTTGGTGGTTCAGGCAACATTTTCAGCAGGCTGCTGCTCAACAGTGGATGCAAA	960
DB	901	CTATATGTTGGTGGTTCAGGCAACATTTTCAGCAGGCTGCTGCTCAACAGTGGATGCAAA	960
QY	961	GTAAGCGGAAACCTTTCAGCAAGCAAGAAATTTAGTACTCAAAACACCTTTGA	1014
DB	961	GTAAGCGGAAACCTTTCAGCAAGCAAGAAATTTAGTACTCAAAACACCTTTGA	1014

RESULT 4

ABSS1730

ID ABSS1730 standard; cDNA; 1560 BP.

XX AC ABSS1730;

XX DT 21-OCT-2002 (first entry)

XX DE Human novel polynucleotide #3.

XX KW Human; gene; ss; trauma; viral infection; parasitic infection; addiction;  
bacterial infection; Alzheimer's disease; Huntington's disease; anxiety;  
Parkinson's disease; behavioral disorder; pain; hair growth disease;  
alopecia; pigmentary disorder; inflammatory disorder; arthritis; AIDS;  
inflammatory bowel disease; Crohn's disease; cancer; adenocarcinoma;  
acquired immunodeficiency syndrome; colon; asthma; hypertension; obesity;  
autoimmune disease; diabetes; graft versus host disease; ulcer; bulimia;  
anorexia; dementia; gene therapy.

XX OS Homo sapiens.

XX PN WO200257452-A2.

XX PD 25-JUL-2002.

XX PF 17-DEC-2001; 2001WO-US049122.

XX PR 15-DEC-2000; 2000US-0256025P.

XX PR 30-JAN-2001; 2001US-0265163P.

XX PR 02-MAR-2001; 2001US-0272929P.

XX PR 09-MAR-2001; 2001US-0274864P.

XX PR 16-MAR-2001; 2001US-0276688P.

XX PR 22-MAR-2001; 2001US-0277880P.

XX PR 25-APR-2001; 2001US-0286409P.

XX PR 31-JUL-2001; 2001US-0309246P.

XX PR 29-AUG-2001; 2001US-0315600P.

XX (CURA-) CURAGEN CORP.

XX PA Shimketa RA, Coleman SD, Spytke KA, Ballinger RA, Guo X;

XX PI Tchernev VT, Shenoy SG, Li L, Ellerman KE, Zerhusen BD;

XX PI Patturajan M, Casman SJ, Boldog F, Gusev VI, Burgess CE, Edinger S;

XX PI Gangolli EA, Malyankar UM, Gunther E, Smithson G, Millet I;

XX PI Gerlach VL;

XX DR WPI; 2002-590743/63.

XX DR P-PSDB; ABG70287.

Novel polypeptide, designated NOVX for treating or preventing disorders  
or symptoms e.g. trauma, Alzheimer's disease, cancers, acquired  
immunodeficiency syndrome, asthma and rheumatoid arthritis.

Claim 9; Page 25; 252pp; English.



The invention relates to human novel polynucleotides and polypeptides. The sequences are useful for the treatment, prevention and diagnosis of disorders such as trauma, viral/parasitic/bacterial infections, Alzheimer's disease, Huntington's disease, Parkinson's disease, behavioural disorders, anxiety, addiction, pain, hair growth diseases, alopecia, pigmentation disorder, inflammatory disorders such as osteoarthritis, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, acquired immunodeficiency syndrome (AIDS), cancers such as colon cancer and adenocarcinoma, asthma, hypertension, autoimmune disease, diabetes, obesity, graft versus host disease, ulcer, bulimia, anorexia and dementia. Sequences ABS51728-ABS51748 represent human novel polynucleotides of the invention

Query Match 100.0%; Score 1014; DB 6; Length 1560; Best Local Similarity 100.0%; Pred. No. 2.4e-289; Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTTATGCGCTGCT 60  
 Db ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTTATGCGCTGCT 412

QY 61 TTTGGAATGCACTGATGAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
 Db TTTGGAATGCACTGATGAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 472

QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180  
 Db GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 532

QY 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG 240  
 Db AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG 592

QY 241 CTGTATCTGACGACCTCCCTTCTGATTCATCTACTATGCCAGTGGGAAAACTGGATC 300  
 Db CTGTATCTGACGACCTCCCTTCTGATTCATCTACTATGCCAGTGGGAAAACTGGATC 652

QY 301 TTTGGAGATTTCAATGTTAAGTTTATCCGCTTCAGCTTCCATTCACCTGTATAGCAGC 360  
 Db TTTGGAGATTTCAATGTTAAGTTTATCCGCTTCAGCTTCCATTCACCTGTATAGCAGC 712

QY 361 ATCCTCTTCTCACCCTGTTTACGATCTTCCGCTACTGTGTATCATTCACCCAAATGAGC 420  
 Db ATCCTCTTCTCACCCTGTTTACGATCTTCCGCTACTGTGTATCATTCACCCAAATGAGC 772

QY 421 TGCCTTTTCCATTCAAAACTCGATGTCAGTTGTAGCTGTGCTGTGGTGTGGATCATTT 480  
 Db TGCCTTTTCCATTCAAAACTCGATGTCAGTTGTAGCTGTGCTGTGGTGTGGATCATTT 832

QY 481 TCAGTGTGTGCTGATTCCTCGATGACCTTCTTGATCACATCAACCAAGGACCAACAGA 540  
 Db TCAGTGTGTGCTGATTCCTCGATGACCTTCTTGATCACATCAACCAAGGACCAACAGA 892

QY 541 TCAGCTGTCTGACCTCAACGATTCGGATGAATCAATTAATTAAGTGTGTAACACCTA 600  
 Db TCAGCTGTCTGACCTCAACGATTCGGATGAATCAATTAATTAAGTGTGTAACACCTA 952

QY 601 ATTTTGACTGCACTACTTCTTCCCTCCCTGGTGATGATGACACTTTGCTATACCAAG 660  
 Db ATTTTGACTGCACTACTTCTTCCCTCCCTGGTGATGATGACACTTTGCTATACCAAG 1012

QY 661 ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 720  
 Db ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 1072

QY 721 AGGCTAACCACTTCTGCTACTCTTCTGCAATTTACGATGTTTTTACCTTCCATATCTTG 780  
 Db AGGCTAACCACTTCTGCTACTCTTCTGCAATTTACGATGTTTTTACCTTCCATATCTTG 1132

QY 781 AGGTCATTCGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTCAGAAATCAGATC 840  
 Db AGGTCATTCGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTCAGAAATCAGATC

Db 1133 AGGTCATTCGATCGAATCTCGCTGCTTTCATCATGATGTTTCCATTCAGAAATCAGATC 1192  
 QY 841 CATGAACCTTACATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
 Db 1193 CATGAACCTTACATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAACTGTTA 1252  
 QY 901 CTATATGCTGTGGTGCAGCAACTTTTCAGCAGGCTCTGCTCAACAGTGGAGTCAAA 960  
 Db 1253 CTATATGCTGTGGTGCAGCAACTTTTCAGCAGGCTCTGCTCAACAGTGGAGTCAAA 1312  
 QY 961 GTAAGCGGGAACCTTGAGCAAGCAAAAGAAAATAGTTTACTCAAAACACCTTTGA 1014  
 Db 1313 GTAAGCGGGAACCTTGAGCAAGCAAAAGAAAATAGTTTACTCAAAACACCTTTGA 1366

RESULT 5  
 ABS51678  
 ID ABS51678 standard; DNA; 1851 BP.

XX AC ABS51678;  
 XX AC  
 DT 05-NOV-2002 (first entry)

XX DNA encoding human Purinoceptor-like protein.  
 DE Human; NOVX; pathological condition; NOVX-associated disorder;  
 XX Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;  
 KW pancreatitis; obesity; diabetes; autoimmune disease; infertility;  
 KW renal artery stenosis; interstitial nephritis; glomerulonephritis;  
 KW polycystic kidney disease; cataract; Alzheimer's disease; cancer;  
 KW acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;  
 KW congenital heart defect; scleroderma; endometriosis; haemophilia;  
 KW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;  
 KW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;  
 KW acne; wound; asthma; human disease; calpain; epsin; zinc finger;  
 KW low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;  
 KW serine protease TLSP; mitogen activated protein kinase kinase-2;  
 KW glypican-2 precursor; thymosin beta-10; gene; ds.

XX Homo sapiens.  
 OS  
 XX  
 PN MO200255702-A2.  
 XX  
 PD 18-JUL-2002.  
 XX  
 PF 26-OCT-2001; 2001WO-US050925.  
 XX  
 PR 26-OCT-2000; 2000US-0243320P.  
 PR 26-OCT-2000; 2000US-0243592P.  
 PR 26-OCT-2000; 2000US-0243642P.  
 PR 27-OCT-2000; 2000US-0243681P.  
 PR 27-OCT-2000; 2000US-0243683P.  
 PR 31-OCT-2000; 2000US-0244443P.  
 PR 01-NOV-2000; 2000US-0244995P.  
 PR 01-NOV-2000; 2000US-0245029P.  
 PR 02-NOV-2000; 2000US-0245293P.  
 PR 02-NOV-2000; 2000US-0245315P.  
 PR 02-NOV-2000; 2000US-0245316P.  
 PR 19-JAN-2001; 2001US-0262994P.  
 PR 15-FEB-2001; 2001US-0269056P.  
 PR 02-MAR-2001; 2001US-0272923P.  
 PR 15-MAR-2001; 2001US-0276565P.  
 PR 07-SEP-2001; 2001US-0318119P.  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Gangolli EA, Spytek KA, Gilbert J, Casman S, Blalock A, Li L;  
 PI Vernet CM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;  
 PI Malyankar U, Stone D, Millet I, Smithson G, Gunther E, Padigar M;  
 PI Taupier RJ, Anderson D;  
 XX WPI; 2002-590673/63.  
 DR P-PSDB; ABG70271.

XX Isolated NOVX polypeptides and nucleic acid molecules useful for  
PT treating, preventing, diagnosing and researching pathological conditions  
PT in humans with a NOVX-associated disorders, e.g. cancer, stroke or  
PT Alzheimer's disease.  
XX  
PS Claim 8; Page 32; 236pp; English.  
XX  
CC The present invention relates to a new polypeptide that comprises any of  
CC 17 fully defined sequences of 43-990 amino acids given in the  
CC specification. The NOVX polypeptide, nucleic acid and antibody of the  
CC invention are useful for treating or preventing a pathological condition  
CC in humans with a NOVX-associated disorder, e.g. Von Hippel-Lindau  
CC syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,  
CC diabetes, autoimmune disease, renal artery stenosis, interstitial  
CC nephritis, glomerulonephritis, polycystic kidney disease, cataract,  
CC Alzheimer's disease, acoustic trauma, cancer, infertility,  
CC cardiomyopathies, atherosclerosis, hypertension, congenital heart  
CC defects, scleroderma, endometriosis, haemophilia, dementia, stroke,  
CC Parkinson's disease, Huntington's disease, epilepsy, multiple sclerosis,  
CC anxiety, pain, leukaemia, hypothyroidism, psoriasis, acne, wounds and  
CC asthma. They are also useful for the manufacture of a medicament for  
CC treating a syndrome associated with a human disease, specifically a NOVX-  
CC associated disorder. They may also be useful in therapeutic applications  
CC including protein therapy, as small molecule drug targets, as antibody  
CC targets, as diagnostic and/or prognostic markers, in gene therapy, as  
CC research tools and in tissue regeneration. The present nucleic acid  
CC sequence encodes one of the 17 novel proteins of the invention  
XX  
SQ Sequence 1851 BP; 509 A; 458 C; 341 G; 543 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 6; Length 1851;  
Best Local Similarity 100.0%; Pred. No. 2.6e-289;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCGTATTTCCCGGATTATGAGCTGCT 60  
DB 347 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCGTATTTCCCGGATTATGAGCTGCT 406  
QY 61 TTTGGAAATGCTGATGAACATCCCACTCAAGATGCTACTCCCTGTTATTTAT 120  
DB 407 TTTGGAAATGCTGATGAACATCCCACTCAAGATGCTACTCCCTGTTATTTAT 466  
QY 121 GCAATATCTTCTCTGTTGATTTCCAGGCAATGCTAGTATGATATCCACTTACATTTTC 180  
DB 467 GCAATATCTTCTCTGTTGATTTCCAGGCAATGCTAGTATGATATCCACTTACATTTTC 526  
QY 181 AAAATGAGACCTTTGGAAGAGCAGCACATCATTTATGCTGAACTGGCCCTGCACAGATCTG 240  
DB 527 AAAATGAGACCTTTGGAAGAGCAGCACATCATTTATGCTGAACTGGCCCTGCACAGATCTG 586  
QY 241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300  
DB 587 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 646  
QY 301 TTTGGAGATTTCAATGTTAGTTTATTCGGTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
DB 647 TTTGGAGATTTCAATGTTAGTTTATTCGGTTTCAGCTTCCATTTCAACCTGTATAGCAGC 706  
QY 361 ATCCCTCTTCTACCTGTTTTCAGATCTTCCGCTACTGTGTATCATCCCAATGAGC 420  
DB 707 ATCCCTCTTCTACCTGTTTTCAGATCTTCCGCTACTGTGTATCATCCCAATGAGC 766  
QY 421 TGCTTTTCCATTCACAAATCCGATGTCAGTTGTAGCTGTGCTGGTGTGGATCAT 480  
DB 767 TGCTTTTCCATTCACAAATCCGATGTCAGTTGTAGCTGTGCTGGTGTGGATCAT 826  
QY 481 TCACTGTAGTGTGCTATTCGATGACCTTCTTGTATCATCAACCAACAGGACCAACAGA 540  
DB 827 TCACTGTAGTGTGCTATTCGATGACCTTCTTGTATCATCAACCAACAGGACCAACAGA 886  
QY 541 TCAGCTGTCTCGACCTTCAACAGTTCCGATGAATCAATCACTATTAGTGGTACAACTTA 600

DB 887 TCAGCTGTCTCGACCTTCAACAGTTCCGATGAATCAATCACTATTAGTGGTACAACTTA 946  
QY 601 ATTTTGAAGTCAACTACTTTCTGCTCCCTTGGTATAGTGAACACTTTGATATACACAG 660  
DB 947 ATTTTGAAGTCAACTACTTTCTGCTCCCTTGGTATAGTGAACACTTTGATATACACAG 1006  
QY 661 ATTATCCACACTCTGACCCATGGAAGTCAAACTGACAGCTGCTTAAAGCAAGACAGA 720  
DB 1007 ATTATCCACACTCTGACCCATGGAAGTCAAACTGACAGCTGCTTAAAGCAAGACAGA 1066  
QY 721 AGGTCAACCACTCTGCTACTCTCTGATTTTACGATGATTTTACCTTCCATATCTTG 780  
DB 1067 AGGTCAACCACTCTGCTACTCTCTGATTTTACGATGATTTTACCTTCCATATCTTG 1126  
QY 781 AGGTCACTTCGATGCAATCTCGCTGCTTTCAATCACTGTTTCAATGAGATCAGATC 840  
DB 1127 AGGTCACTTCGATGCAATCTCGCTGCTTTCAATCACTGTTTCAATGAGATCAGATC 1186  
QY 841 CATGAAGCTTACATGCTTTCTAGACCATTTAGACCATTTAGACCATTTAGACCATTTAG 900  
DB 1187 CATGAAGCTTACATGCTTTCTAGACCATTTAGACCATTTAGACCATTTAGACCATTTAG 1246  
QY 901 CTATATGTTGGTGTGTCAGGCAAACTTTTCAGAGGCTGCTGCTCAACAGTGAAGTCAAA 960  
DB 1247 CTATATGTTGGTGTGTCAGGCAAACTTTTCAGAGGCTGCTGCTCAACAGTGAAGTCAAA 1306  
QY 961 GTAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAACAAACCTTTGA 1014  
DB 1307 GTAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAACAAACCTTTGA 1360  
RESULT 6  
AAS07948  
ID AAS07948 standard; cDNA; 1014 BP.  
XX AAS07948;  
XX  
DT 23-OCT-2001 (first entry)  
XX Human cDNA encoding G-protein coupled receptor, hrUP21.  
DE Human; G-protein coupled receptor; GPCR; hrUP21; agonist;  
KW Inverse agonist; lung cancer; ss.  
XX Homo sapiens.  
OS  
FH Key  
CDS 1..1014  
FT /\*tag= a  
FT /product= "hrUP21"  
XX  
PN WO200136471-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000WO-US031509.  
XX  
PR 17-NOV-1999; 99US-0166088P.  
PR 17-NOV-1999; 99US-0166099P.  
PR 17-NOV-1999; 99US-0166369P.  
PR 23-DEC-1999; 99US-0171900P.  
PR 23-DEC-1999; 99US-0171901P.  
PR 23-DEC-1999; 99US-0171902P.  
PR 11-FEB-2000; 2000US-0181749P.  
PR 14-MAR-2000; 2000US-0189258P.  
PR 14-MAR-2000; 2000US-0189259P.  
PR 10-APR-2000; 2000US-0195898P.  
PR 10-APR-2000; 2000US-0195899P.  
PR 10-APR-2000; 2000US-0196078P.  
PR 28-APR-2000; 2000US-0200419P.  
PR 12-MAY-2000; 2000US-0203630P.  
PR 12-JUN-2000; 2000US-0210741P.  
PR 12-JUN-2000; 2000US-0210982P.

PR 21-AUG-2000; 2000US-0226760P.  
PR 26-SEP-2000; 2000US-0235418P.  
PR 26-SEP-2000; 2000US-0235779P.  
PR 20-OCT-2000; 2000US-0242332P.  
PR 20-OCT-2000; 2000US-0242343P.  
PR 24-OCT-2000; 2000US-0243019P.  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Chen R, Dang HT, Lowitz KP;  
XX  
XX WPI; 2001-355616/37.  
DR F-PSDB; AAU04375.  
XX  
PT Endogenous and non-endogenous versions of human G-protein coupled  
PT receptors for direct identification of candidate compounds as agonists,  
PT inverse agonists or partial agonists for use as therapeutic agents.  
XX  
PS Claim 55; Page 113-114; 160pp; English.  
XX  
CC The sequence encodes a human G-protein coupled receptor (GPCR), hRUP21  
CC The endogenous and non-endogenous, constitutively activated versions of  
CC human G-protein coupled receptors (GPCR), are useful for direct  
CC identification of candidate compounds as receptor agonists, inverse  
CC agonists or partial agonists having applicability as therapeutic agents  
CC for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous  
CC version of human GPCRs are also utilized in research settings and in  
CC vitro and in vivo system, incorporating GPCRs can be utilised to  
CC elucidate and understand the roles these receptors play in the human  
CC condition, both normal and diseased  
XX  
SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 5; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 5.8e-289;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATATGACGCTGT 60  
DB 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATATGACGCTGT 60  
QY 61 TTGGAATGACATGATGAAACATCCCACTCAAGATGACATCTCCCTGTTATTTAT 120  
DB 61 TTGGAATGACATGATGAAACATCCCACTCAAGATGACATCTCCCTGTTATTTAT 120  
QY 121 GSCATTATCTTCTCGTGGATTTCCAGCATGAGTAGTATCATATCCATTTACATTTTC 180  
DB 121 GSCATTATCTTCTCGTGGATTTCCAGCATGAGTAGTATCATATCCATTTACATTTTC 180  
QY 181 AAAATGAGACCTTGAAGAGCAGCACCACATCATTTATGCTGAACCTGGCTGCACAGATCTG 240  
DB 181 AAAATGAGACCTTGAAGAGCAGCACCACATCATTTATGCTGAACCTGGCTGCACAGATCTG 240  
QY 241 CTGATCTGACAGGCTCCCTTCTGATTTCACTATGCGAGTGGGGAACCTGGATC 300  
DB 241 CTGATCTGACAGGCTCCCTTCTGATTTCACTATGCGAGTGGGGAACCTGGATC 300  
QY 301 TTGAGATTTTCACTGTAAGTTTATCGCTTCAGCTTCCATTTCAACTGTATAGCAGC 360  
DB 301 TTGAGATTTTCACTGTAAGTTTATCGCTTCAGCTTCCATTTCAACTGTATAGCAGC 360  
QY 361 ATCTCTTCTCCTCACCCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTTCAACCAATGAGC 420  
DB 361 ATCTCTTCTCCTCACCCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTTCAACCAATGAGC 420  
QY 421 TGCTTTTCCATTTCAAAACTCGATGTGCGAGTTGAGCTGTGCTGTGTGTGATCATTT 480  
DB 421 TGCTTTTCCATTTCAAAACTCGATGTGCGAGTTGAGCTGTGCTGTGTGTGATCATTT 480  
QY 481 TCACGTGGTAGCTGCTATTCGAGTACCTTCTTGATCAGATCAACCAAGGACCAACAGA 540  
DB 481 TCACGTGGTAGCTGCTATTCGAGTACCTTCTTGATCAGATCAACCAAGGACCAACAGA 540

QY 541 TCAGCTGTCTCGACCTCACCAGTTCCGATGAACCTCAATACTATTAAAGTGGTACAACTTA 600  
DB 541 TCAGCTGTCTCGACCTCACCAGTTCCGATGAACCTCAATACTATTAAAGTGGTACAACTTA 600  
QY 601 ATTTGACTGCAACTACTTTTCTGCTTCCCTTCCCTTGGTGATAGTACACTTTTCTATACCA 660  
DB 601 ATTTGACTGCAACTACTTTTCTGCTTCCCTTCCCTTGGTGATAGTACACTTTTCTATACCA 660  
QY 661 ATTATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAAGACAGA 720  
DB 661 ATTATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAAGACAGA 720  
QY 721 AGCTTAACCAATCTGCTACTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780  
DB 721 AGCTTAACCAATCTGCTACTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780  
QY 781 AGGTCATTCGGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTCAGATCAGATC 840  
DB 781 AGGTCATTCGGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTCAGATCAGATC 840  
QY 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAAACACTTTGGTAACTGTTA 900  
DB 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAAACACTTTGGTAACTGTTA 900  
QY 901 CTATATGTGCTGCTGAGCAGCAACTTTTACAGAGGCTGCTGCTCAACAGTGAAGTCAA 960  
DB 901 CTATATGTGCTGCTGAGCAGCAACTTTTACAGAGGCTGCTGCTCAACAGTGAAGTCAA 960  
QY 961 GTAAAGCGGAACTTTGAGCAAGCAAGAAATAGTTACTCAAAACACCTTTGA 1014  
DB 961 GTAAAGCGGAACTTTGAGCAAGCAAGAAATAGTTACTCAAAACACCTTTGA 1014

RESULT 7  
ABN85630  
ID ABN85630 standard; DNA; 1014 BP.  
XX  
AC ABN85630;  
XX  
DT 18-SEP-2002 (first entry)  
XX  
DE Human P2Y-like receptor variant encoding gene SEQ ID NO 3.  
XX  
KW Human; P2Y-like receptor; HIPHUM 000037; immunity; inflammation; cancer;  
KW Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;  
KW immunomodulator; anti-inflammatory; cytostatic; antiasthmatic;  
KW gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide;  
KW antibacterial; immunosuppressive; dermatological; nephrotropic;  
KW antiallergic; analgesic; receptor; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1014  
FT /tag= a  
FT /product= "P2Y-like receptor variant"  
XX  
PN GB2369364-A.  
XX  
XX 29-MAY-2002.  
XX  
XX 31-AUG-2001; 2001GB-00021215.  
XX  
PR 01-SEP-2000; 2000GB-00021524.  
PR 06-SEP-2000; 2000GB-00021894.  
PR 25-SEP-2000; 2000GB-00023444.  
XX  
PA (GLAXO) GLAXO GROUP LTD.  
XX  
XX Foord SM, Ignar DM;  
XX WPI; 2002-511268/55.  
DR P-PSDB; ABB83819.

XX An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can be  
 PT used for the identification of agonists and antagonists which may be used  
 PT to treat an immune or inflammatory disease.

XX Claim 5; Page 28-29; 35pp; English.

XX The invention relates to an isolated P2Y-like receptor polypeptide  
 CC (ABB83818-ABB83819) which is also referred to in the specification as  
 CC HIPHUM 0000037. An effective amount of a substance (agonist or  
 CC antagonist) which modulates P2Y receptor activity is useful to treat a  
 CC subject having a disorder that is responsive to P2Y-like receptor  
 CC modulation. The disorder is a disease of immunity or inflammation. The  
 CC substance may also be used to manufacture a medicine for the treatment or  
 CC prophylaxis of a disorder that is responsive to stimulation or modulation  
 CC of P2Y-like receptor activity. Disorders which may be treated include  
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,  
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative  
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,  
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic  
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,  
 CC polymyositis or prostatitis. The invention provides alternative  
 CC substances for the treatment of immunological and inflammatory diseases.  
 CC The present sequence is that the P2Y-like receptor variant encoding gene  
 CC of the invention

XX SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;  
 Best Local Similarity 99.9%; Pred. No. 5.8e-289;  
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCAGTACATATTAGCAAAATGCTCTGATTTCCCGGATTTATGACGCTGCT 60  
 DB 1 ATGAATGAGCAGTACATATTAGCAAAATGCTCTGATTTCCCGGATTTATGACGCTGCT 60

QY 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
 DB 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120

QY 121 GGCATTATCTTCCTCGTGGGATTTCCAGCAATGCACTAGTATGATACCACTACATTTTC 180  
 DB 121 GGCATTATCTTCCTCGTGGGATTTCCAGCAATGCACTAGTATGATACCACTACATTTTC 180

QY 181 AAATGAGACCTTGGAGAGCAGCAGCACCATTATGCTGAACTGGCTGACAGATCTG 240  
 DB 181 AAATGAGACCTTGGAGAGCAGCAGCACCATTATGCTGAACTGGCTGACAGATCTG 240

QY 241 CTGTATCTGACAGCCTCCCTTCCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300  
 DB 241 CTGTATCTGACAGCCTCCCTTCCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300

QY 301 TTGGAGATTTGATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACTGTATAGCAGC 360  
 DB 301 TTGGAGATTTGATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACTGTATAGCAGC 360

QY 361 ATCCCTCTCCTCACTGTTTTCAGCATCTTCGCTACTGTCATCATTCACCCCAATGAGC 420  
 DB 361 ATCCCTCTCCTCACTGTTTTCAGCATCTTCGCTACTGTCATCATTCACCCCAATGAGC 420

QY 421 TGCTTTTCCATTCACAAATCGATGTCAGTGTGAGCTGTGCTGTGTCGATTCATT 480  
 DB 421 TGCTTTTCCATTCACAAATCGATGTCAGTGTGAGCTGTGCTGTGTCGATTCATT 480

QY 481 TCACCTGGTGTGTCATTCGGATGACCTTCTTGTATCAGATCAATCAACAGGACCAACAGA 540  
 DB 481 TCACCTGGTGTGTCATTCGGATGACCTTCTTGTATCAGATCAATCAACAGGACCAACAGA 540

QY 541 TCAGCTGTCTCGACCTCCACAGTTCGGATGACCTCAATCAATCAATCAATCAATCAATCA 600  
 DB 541 TCAGCTGTCTCGACCTCCACAGTTCGGATGACCTCAATCAATCAATCAATCAATCAATCA 600

QY 601 ATTTGACTGCAACTACTTTCTGCTCCCTGCTGGTATGATGACACTTTGCTATACCAGC 660

DB 601 ATTTGACTGCAACTACTTTCTGCTCCCTGCTGGTATGATGACACTTTGCTATACCAGC 660  
 QY 661 ATTTGACTGCAACTACTTTCTGCTCCCTGCTGGTATGATGACACTTTGCTATACCAGC 720  
 DB 661 ATTTGACTGCAACTACTTTCTGCTCCCTGCTGGTATGATGACACTTTGCTATACCAGC 720  
 QY 721 AGGCTAACCACTTCTGCTACTCTCTTTCGATTTTACGATTTTACCTTCCATATCTTG 780  
 DB 721 AGGCTAACCACTTCTGCTACTCTCTTTCGATTTTACGATTTTACCTTCCATATCTTG 780

QY 781 AGGCTCAATGCGATGCAATCTGCTGCTTTCATCACTGCTTTCATGAGATGAGATCAGATC 840  
 DB 781 AGGCTCAATGCGATGCAATCTGCTGCTTTCATCACTGCTTTCATGAGATGAGATCAGATC 840

QY 841 CATCAAGCTTACATCGTTTCTAGACCACTTACCTGCTCTGAAACACCTTTGGTAACTGTTA 900  
 DB 841 CATCAAGCTTACATCGTTTCTAGACCACTTACCTGCTCTGAAACACCTTTGGTAACTGTTA 900

QY 901 CTATATGCTGGTGGTCAAGCAAACTTTTCAGCAGCTGCTGCTCAACAGTGAAGATGAAA 960  
 DB 901 CTATATGCTGGTGGTCAAGCAAACTTTTCAGCAGCTGCTGCTCAACAGTGAAGATGAAA 960

QY 961 GTAAAGCGGACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014  
 DB 961 GTAAAGCGGACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 8  
 AAK98323

ID AAK98323 standard; cDNA; 1014 BP.

XX AAK98323;

DT 30-APR-2002 (first entry)

DE Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.

XX Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;  
 KW signal transduction; human protease; GPCR disorder; gene therapy;  
 KW transgenic animal; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1014

XX /tag= a

XX /product= "G-protein coupled receptor"

XX WO200187980-A2.

XX 22-NOV-2001.

XX 17-MAY-2001; 2001WO-US015957.

XX 18-MAY-2000; 2000US-0205196P.

XX 08-AUG-2000; 2000US-00634656.

XX (APPL-) APPLERA CORP.

XX Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;

XX WPI; 2002-075312/10.

XX P-PSDB; AAO14027.

XX Novel isolated G-protein coupled receptor peptide useful for treating  
 PT disorder characterized by absence of, in appropriate or unwanted  
 PT expression of the receptor protein, and as immunogens to raise  
 PT antibodies.

XX Claim 23; Fig 1; 64pp; English.

XX The present specifically claimed human cDNA sequence (located on

chromosome 13) encodes a purinergic-related G-protein coupled receptor (GPCR) of the invention. GPCRs constitute a major class of proteins responsible for signal transduction within a cell. Upon binding of a ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The GPCR proteins can be divided into five families, family I contains the purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are characterised by their selective responsiveness towards ATP and its analogues, some also respond to UTP. The invention comprises a human G-protein coupled receptor protein and encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein of the invention is useful for: the development/identification of therapeutic proteins; assays designed to quantitatively determine levels of the protein in biological fluids; identifying compounds which modulate the activity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR nucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; controlling GPCR expression; and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals

Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;  
 Best Local Similarity 99.9%; Pred. No. 5.8e-289;  
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCAGCTAGCTATTTAGCAAAATGCTTCTGATTTCCCGGATTTATGCTGCT 60  
 DB 1 ATGAATGAGCAGCTAGCTATTTAGCAAAATGCTTCTGATTTCCCGGATTTATGCTGCT 60

QY 61 TTTGGAATTTGCACTGATGAAACATCCCACTCAAGATGCATCTCCCTGTTATTTAT 120  
 DB 61 TTTGGAATTTGCACTGATGAAACATCCCACTCAAGATGCATCTCCCTGTTATTTAT 120

QY 121 GSCATTTATCTTCCTCGTGGGATTTCCAGGCAATGCGATGATGATATCCATTTACATTTTC 180  
 DB 121 GSCATTTATCTTCCTCGTGGGATTTCCAGGCAATGCGATGATGATATCCATTTACATTTTC 180

QY 181 AAATGAGACCTTGAAGAGCAGCAGCACCATTATGCTGAACTGGCCCTGCACAGATCTG 240  
 DB 181 AAATGAGACCTTGAAGAGCAGCAGCACCATTATGCTGAACTGGCCCTGCACAGATCTG 240

QY 241 CTGTATCTGACAGCCTCCCTTCCGTGATTCATCTACTATGCGAGTGGGAAACTGGATC 300  
 DB 241 CTGTATCTGACAGCCTCCCTTCCGTGATTCATCTACTATGCGAGTGGGAAACTGGATC 300

QY 301 TTTGAGATTTTCATGTGAAGTTTATCCGCTTCAGCTTCCATCTGATAGCAGC 360  
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QY 361 ATCTCTTCTCAGCTGTTTTCAGCATCTTCGCTACTGTGATCATTCACCAATGAGC 420  
 DB 361 ATCTCTTCTCAGCTGTTTTCAGCATCTTCGCTACTGTGATCATTCACCAATGAGC 420

QY 421 TGCTTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGCTGCTGTGATCATTT 480  
 DB 421 TGCTTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGCTGCTGTGATCATTT 480

QY 481 TCATGCTAGTGTGATTCATTCGAGTACCTTCTTGATCAGATCAATCAACCAAGACCAACAGA 540  
 DB 481 TCATGCTAGTGTGATTCATTCGAGTACCTTCTTGATCAGATCAATCAACCAAGACCAACAGA 540

QY 541 TCAGCTGTCTGAGCCTCACCAGTTCGGATGATCAATCAATTAAGTGTGATCAACCTA 600  
 DB 541 TCAGCTGTCTGAGCCTCACCAGTTCGGATGATCAATCAATTAAGTGTGATCAACCTG 600

QY 601 ATTTGACTGCAACTACTTCTGCTCCCTGCTGATGATGACACTTTGCTATACACG 660  
 DB 601 ATTTGACTGCAACTACTTCTGCTCCCTGCTGATGATGACACTTTGCTATACACG 660

QY 661 ATTATCCACACTGACCCATGACCTGCAAACTGACAGCTGCTTAAAGCAGAACGACGA 720  
 DB 661 ATTATCCACACTGACCCATGACCTGCAAACTGACAGCTGCTTAAAGCAGAACGACGA 720

QY 721 AGGCTAAACCAATCTGCTACTCTCTTGCATTTTACGATGTTTACCTTCCATATCTTG 780  
 DB 721 AGGCTAAACCAATCTGCTACTCTCTTGCATTTTACGATGTTTACCTTCCATATCTTG 780

QY 781 AGGCTCAATTCGGATGAAATCTCGCTGCTTTCAATCAGTTGTTTCCATGAGATCAGATC 840  
 DB 781 AGGCTCAATTCGGATGAAATCTCGCTGCTTTCAATCAGTTGTTTCCATGAGATCAGATC 840

QY 841 CATGAGCTTTACATCGTTTCTAGACCAATGAGTCTGCAACACCTTTGGTAACCTGTTA 900  
 DB 841 CATGAGCTTTACATCGTTTCTAGACCAATGAGTCTGCAACACCTTTGGTAACCTGTTA 900

QY 901 CTATATGCTGCTGTCAGCGACAACTTTTCAGCAGGCTGCTGCTCAACACTGAGATCAAA 960  
 DB 901 CTATATGCTGCTGTCAGCGACAACTTTTCAGCAGGCTGCTGCTCAACACTGAGATCAAA 960

QY 961 GTAAGCGGAACTTTCAGCAAGCAAAAGAAATAGTTACTCAAAACACCTTTGA 1014  
 DB 961 GTAAGCGGAACTTTCAGCAAGCAAAAGAAATAGTTACTCAAAACACCTTTGA 1014

RESULT 9  
 ABK11381  
 ID ABK11381 standard; DNA; 1014 BP.  
 XX  
 AC ABK11381;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Human DNA encoding P2Y1-like G protein-coupled receptor.  
 XX  
 KW Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR; infection;  
 KW pain; cancer; anorexia; bulimia; asthma; hypotension;  
 KW central nervous system disease; acute heart failure; hypertension;  
 KW urinary retention; osteoporosis; diabetes; angina pectoris;  
 KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;  
 KW benign prostatic hypertrophy; psychosis; neurological disorder;  
 KW dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;  
 KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;  
 KW dementia; severe mental retardation; Huntington's disease;  
 KW Tourette's syndrome.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1014  
 FT /\*tag= a  
 FT /product= "P2Y1-like GPCR"  
 XX  
 PN WO200214511-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-EP009243.  
 XX  
 PR 14-AUG-2000; 2000US-0224989P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Ramakrishnan S;  
 XX  
 DR WPI; 2002-257607/30.  
 XX  
 DR P-PSDB; AAU77600.  
 XX  
 PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can be  
 PT regulated for treating infection, pain, cancer, diabetes, anorexia,  
 PT asthma, hypertension, neurological disorder and dyskinesia.  
 XX

PS	Claim 1; Fig 5; 118pp; English.	
XX	The invention relates to a purified human P2Y <sub>1</sub> -like G protein-coupled	
CC	receptor (GPCR) polypeptide and the nucleic acids encoding it (including	
CC	5' and 3' sequences, promoters, fragments, variants, or a sequence	
CC	encoding a protein at least 50% identical to the GPCR). Also included are	
CC	an expression vector comprising the nucleic acid, a host cell containing	
CC	the vector and the identification of modulators of the GPCR especially	
CC	those that reduce the activity of the GPCR. The nucleic acid is useful	
CC	for detecting a polynucleotide encoding the GPCR in a biological sample.	
CC	The GPCR and nucleic acid are useful for screening for agents which	
CC	decrease the activity of the GPCR and for modulators of the GPCR. The	
CC	modulator or agent useful for modulating the activity of P2Y <sub>1</sub> -like G	
CC	protein-coupled receptor in a disease such as bacterial, fungal,	
CC	protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma,	
CC	central nervous system (CNS) disease, acute heart failure, hypotension,	
CC	hypertension, urinary retention, osteoporosis, diabetes, angina pectoris,	
CC	myocardial infarction, ulcer, inflammation, allergy, multiple sclerosis,	
CC	benign prostatic hypertrophy, psychotic and neurological disorders,	
CC	dyskinesias, HIV virus infection (human immunodeficiency virus), CNS	
CC	disorders such as Parkinson's disease, anxiety, schizophrenia, manic	
CC	depression, delirium, dementia, severe mental retardation, Huntington's	
CC	disease and Tourette's syndrome. The present sequence encodes the P2Y <sub>1</sub> -	
CC	like GPCR of the invention	
XX		
SQ	Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;	
	Query Match 99.8%; Score 1012.4; DB 6; Length 1014;	
	Best Local Similarity 99.9%; Pred. No. 5.8e-289;	
	Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 ATGAATGAGCAGCTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGACGCTGCT 60	
Db	1 ATGAATGAGCAGCTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGACGCTGCT 60	
Qy	61 TTTGGAATTCGACTGATGAAACATCCACTCAAGATGCACTACTCCCTGTTATTAT 120	
Db	61 TTTGGAATTCGACTGATGAAACATCCACTCAAGATGCACTACTCCCTGTTATTAT 120	
Qy	121 GGCATTATCTCTCGTGGGATTTCCAGGATGAGTATGATATCCACTTACATTTTC 180	
Db	121 GGCATTATCTCTCGTGGGATTTCCAGGATGAGTATGATATCCACTTACATTTTC 180	
Qy	181 AAATGAGACCTTGAAGAGCAGCAGCATTATGCTGAACCTGGCCTGCACAGATCTG 240	
Db	181 AAATGAGACCTTGAAGAGCAGCAGCATTATGCTGAACCTGGCCTGCACAGATCTG 240	
Qy	241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300	
Db	241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300	
Qy	301 TTTGGAGATTTTCATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360	
Db	301 TTTGGAGATTTTCATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360	
Qy	361 ATCTCTTCTCCCTCAGCTTTTACGATCTTCCGCTACTGTGATCAITTCACCCATGAGC 420	
Db	361 ATCTCTTCTCCCTCAGCTTTTACGATCTTCCGCTACTGTGATCAITTCACCCATGAGC 420	
Qy	421 TGCTTTTTCATTCACAAACTCGATGTCAGTTGAGCTGTGCTGTGTTGTTGATCAT 480	
Db	421 TGCTTTTTCATTCACAAACTCGATGTCAGTTGAGCTGTGCTGTGTTGTTGATCAT 480	
Qy	481 TCATGGTGTAGCTGATTCGATGATCTTCTGATCAATCAACCAAGGACCAACAGA 540	
Db	481 TCATGGTGTAGCTGATTCGATGATCTTCTGATCAATCAACCAAGGACCAACAGA 540	
Qy	541 TCAGCTGTCTCGACCTCAGCTTCCGATGAACTCAATATTAAGTGGTACACCTTA 600	
Db	541 TCAGCTGTCTCGACCTCAGCTTCCGATGAACTCAATATTAAGTGGTACACCTTA 600	
Qy	601 ATTTGACTGCAACTACTTCTGCTCCCTTGGTGTAGTACACTTTGCTATACACG 660	
Db	601 ATTTGACTGCAACTACTTCTGCTCCCTTGGTGTAGTACACTTTGCTATACACG 660	
Db	601 ATTTGACTGCAACTACTTCTGCTCCCTTGGTGTAGTACACTTTGCTATACACG 660	
Qy	661 ATTATCCACACTCTGACCCATGCAAACTGACAGCTGCTTAAAGCAAGACAGA 720	
Db	661 ATTATCCACACTCTGACCCATGCAAACTGACAGCTGCTTAAAGCAAGACAGA 720	
Qy	721 AGCTTAACCACTTCTGCTTACTCCTTGCATTTTACGATGTTTACCCCTTCCATATCTTG 780	
Db	721 AGCTTAACCACTTCTGCTTACTCCTTGCATTTTACGATGTTTACCCCTTCCATATCTTG 780	
Qy	781 AGGTCATTCGGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTGAGATCAGATC 840	
Db	781 AGGTCATTCGGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTGAGATCAGATC 840	
Qy	841 CATGAACCTTACATCGCTTCTAGACCAATTAGCTCTCTGAACACCTTTGGTAACTGTTA 900	
Db	841 CATGAACCTTACATCGCTTCTAGACCAATTAGCTCTCTGAACACCTTTGGTAACTGTTA 900	
Qy	901 CTATATCTGTTGTTGTCAGCGCAACTTTTACGAGGCTGTCTGCTCAACAGTGAATGCAAA 960	
Db	901 CTATATCTGTTGTTGTCAGCGCAACTTTTACGAGGCTGTCTGCTCAACAGTGAATGCAAA 960	
Qy	961 GTAAGCGGAGACCTTGAAGCAAGCAAAATTTAGTTACTCAAAACACCTTTGA 1014	
Db	961 GTAAGCGGAGACCTTGAAGCAAGCAAAATTTAGTTACTCAAAACACCTTTGA 1014	
DE	Human GPCR polynucleotide SEQ ID NO 13.	
XX	Human; GPCR; G protein coupled receptor; signal transduction; olfactory;	
KW	drug development; gustatory; taste; fragrance; gene; ds.	
OS	Homo sapiens.	
XX	WO200216548-A2.	
PN	28-FEB-2002.	
PD	30-JUL-2001; 2001WO-1B001446.	
PF	04-AUG-2000; 2000JP-00237818.	
PR	13-FEB-2001; 2001JP-00034434.	
XX	(NISC-) JAPAN SCI & TECHNOLOGY CORP.	
PA	Haga T, Takeda S, Mitaku S;	
PI	WPI; 2002-304118/34.	
XX	P-PSDB; ABP95602.	
DR	Database global search for G protein-coupled receptors, proteins and	
XX	encoded genes for studying in vivo signal transduction mechanism and	
PT	identifying targets for drug development.	
PT	Claim 9; SEQ ID NO 13; 97pp + Sequence Listing; Japanese.	
XX	The invention relates to a method for screening G protein-coupled	
CC	receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-	
CC	ABP95942) by extracting open-reading frames containing 6-8 transmembrane	
CC	domains with 250-1000 amino acid residues to give a gene homologous with	
CC	a known GPCR gene. The receptor proteins and encoded genes are useful for	
CC	studying in vivo signal transduction mechanism and identifying targets	
CC	for drug development e.g. based on olfactory and gustatory receptors in	
CC	form of agonists and antagonists by screening intrinsic and extrinsic	
CC	ligands as bitter taste inhibitors, taste enhancers and fragrance	



CC improvers. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 5.8e-289;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATATGCGAGTGTCT 60
DB 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATATGCGAGTGTCT 60

QY 61 TTTGGAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTATTAT 120
DB 61 TTTGGAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTATTAT 120

QY 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGCAATGCAATGCAATGCAATGCAATGCA 180
DB 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGCAATGCAATGCAATGCAATGCAATGCA 180

QY 181 AAAATGAGACCTTGGAGAGCAGCAGCATATATGCTGAACCTGGCCTGCACAGATCTG 240
DB 181 AAAATGAGACCTTGGAGAGCAGCAGCATATATGCTGAACCTGGCCTGCACAGATCTG 240

QY 241 CTGTATCTGACGAGCTCCCTCTCTGATTTCACTACTATGCGAGTGGCGAAACTCGATC 300
DB 241 CTGTATCTGACGAGCTCCCTCTCTGATTTCACTACTATGCGAGTGGCGAAACTCGATC 300

QY 301 TTTGAGATTTCAATGTTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAG 360
DB 301 TTTGAGATTTCAATGTTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAG 360

QY 361 ATCCCTCTCTCCTCCTGTTTTCAGCATTTCCGCTACTGTGTATGATCAATCACCAGAG 420
DB 361 ATCCCTCTCTCCTCCTGTTTTCAGCATTTCCGCTACTGTGTATGATCAATCACCAGAG 420

QY 421 TGCTTTTCCATTCACAAAACCTCGATGCGAGTTGTAGCTGTGCTGTGTGTGTGATTCATT 480
DB 421 TGCTTTTCCATTCACAAAACCTCGATGCGAGTTGTAGCTGTGCTGTGTGTGTGATTCATT 480

QY 481 TCAGTGTAGTGTGATTCGAGACCTTCTTGTATCACAATCAACCAAGAGCCACACAGA 540
DB 481 TCAGTGTAGTGTGATTCGAGACCTTCTTGTATCACAATCAACCAAGAGCCACACAGA 540

QY 541 TCAGCTGTCTGAGCTCAGCTCAGCTGCGATGCACTCAATCACTATTAAAGTGTACACCTA 600
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QY 601 ATTTTGACTGCAACTACTTTCTGCTCCCTCTGGTGATAGTGACACTTTTGTATACCA 660
DB 601 ATTTTGACTGCAACTACTTTCTGCTCCCTCTGGTGATAGTGACACTTTTGTATACCA 660

QY 661 ATTATCCACACTCTGACCACTGAGCTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720
DB 661 ATTATCCACACTCTGACCACTGAGCTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720

QY 721 AGGCTAACCACTCTGCTACTCTGCTGATTTTACGATGATGTTTACCTTCCATATCTTG 780
DB 721 AGGCTAACCACTCTGCTACTCTGCTGATTTTACGATGATGTTTACCTTCCATATCTTG 780

QY 781 AGGGTCATTTCGATCGAATCTCGCTCTCTTCAATCAGTTGTTTCAATTCAGAAATCAGATC 840
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DB 841 CATGAAGCTTACATGTTTCTAGACCAATGCTGCTTCAACACCTTTGTTACCTGTTA 900

QY 901 CTATATGTTGGTTCAGCAGCAACTTTTACAGAGGCTGTCTGCTCAACAGTGTAGTGCMAA 960
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QY 961 GTAAGCGGAACTTGCAGCAAGCAAAAGAAATAGTTACTCAAAACACCTTGA 1014  
DB 961 GTAAGCGGAACTTGCAGCAAGCAAAAGAAATAGTTACTCAAAACACCTTGA 1014

## RESULT 11

ABZ59170  
ID ABZ59170 standard; DNA; 1014 BP.

XX AC ABZ59170;

XX DT 28-APR-2003 (first entry)

DE Human TGR164 protein encoding DNA.

XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;  
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic;  
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;  
XX immunosuppressive; antiinflammatory; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1. .1014  
FT CDS /\*tag= a  
FT /\*product= "TGR164"

XX WO2003004678-A2.

XX 16-JAN-2003.

XX 01-JUL-2002; 2002WO-US020860.

XX 03-JUL-2001; 2001US-0302800P.

XX (TULA-) TULARIK INC.

XX Tian H, Dai K, Chen J, Zhao J, Cutler G;

XX WPI; 2003-210368/20.

XX P-PSDB; ABP71377.

XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,  
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs  
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or  
PT nephrolithiasis.

XX Claim 7; Page 60-61; 74pp; English.

XX The invention provides new G-protein coupled receptor (GPCR) polypeptides  
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding  
CC polynucleotides. The polypeptides can be expressed by standard DNA  
CC recombination methodology. The polypeptides are useful for screening or  
CC identifying modulators of GPCR or signal transduction. The modulators of  
CC signal transduction are useful for treating or preventing TGR-associated  
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The  
CC polypeptides are useful as targets for diagnosing or treating e.g.  
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,  
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,  
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute  
CC inflammatory dermatoses. The present sequence represents a human TGR164  
CC protein encoding DNA

SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 8; Length 1014;

Best Local Similarity 99.9%; Pred. No. 5.8e-289;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATATGCGAGTGTCT 60

DB 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATATGCGAGTGTCT 60



Db 1 ATGAATGAGCCACTAGACTATTATTAGCAAAATGCTTCTGATTTCCCGGATTTATGACGCTGCT 60  
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QY 181 AAAATGAGACTTGGAAAGAGCAGCAGCATCATTTATGCTGAACTGGCCCTGCACAGATCTG 240  
Db 181 AAAATGAGACTTGGAAAGAGCAGCAGCATCATTTATGCTGAACTGGCCCTGCACAGATCTG 240  
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Db 301 TTGGAGATTTTCACTGTTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
QY 361 ATCTCTTCTTCCCTGATTTTCCAGCATCTTCGGTACTGTTGATGATTCACCAATGAGC 420  
Db 361 ATCTCTTCTTCCCTGATTTTCCAGCATCTTCGGTACTGTTGATGATTCACCAATGAGC 420  
QY 421 TGCTTTTCCATTTCAAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 480  
Db 421 TGCTTTTCCATTTCAAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 480  
QY 481 TCACGTGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAAGGACCAACAGA 540  
Db 481 TCACGTGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAAGGACCAACAGA 540  
QY 541 TCAGCTGTCTGACCTCACAGTTCCGATGACCTCAATCACTATTAAGTGGTACACCTTA 600  
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Db 721 AGGCTAACATTTCTGCTACTCTTGGATTTTACCTTCCATATCTTTG 780  
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Db 841 CATGAAGCTTACATCTTTTCTAGACCATTTAGCTGCTTGAACACCTTTGTTAACCTGTTA 900  
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Db 901 CTATATGTTGTTGTCAGCAGCAACTTTTACGAGGCTGTTGCTGCTCAACAGTGAAGTCAAA 960  
QY 961 GTAAGCGGAACCTTGAGCAACCAAGAAATTTAGTTACTCAACACACCTTTGA 1014  
Db 961 GTAAGCGGAACCTTGAGCAACCAAGAAATTTAGTTACTCAACACACCTTTGA 1014

RESULT 13

ADC25997

ID ADC25997 standard; DNA; 1014 BP.

XX

AC ADC25997;

XX

DT 18-DEC-2003 (first entry)  
DE Human purinergic receptor P2Y-related GPCRxl0 DNA.  
XX  
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;  
KW anorectic; cardiant; hypotensive; osteopathic; antianginal;  
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;  
KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;  
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;  
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;  
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;  
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;  
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;  
KW human; GPCRxl0; purinergic receptor P2Y; ds; gene; chromosome 13.  
XX  
OS Homo sapiens.  
XX  
FH Location/Qualifiers  
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FT /\*tag= a  
FT /product= "Human purinergic receptor P2Y-related GPCRxl0  
FT /transl\_except= (pos:214..216, aa:Asn)  
FT /transl\_except= (pos:289..291, aa:Asx)  
FT /transl\_except= (pos:694..696, aa:Cys)  
FT /note= "All translation exceptions are present within the  
FT "original" protein CDS"  
XX  
PN US200308080-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 21-JUN-2001; 2001US-00895453.  
XX  
PR 20-JUN-2000; 2000US-0212908P.  
PR 05-DEC-2000; 2000EP-00870289.  
XX  
PA (COMM/) COMMUNI D.  
PA (LANN/) LANNY V.  
PA (GOVA/) GOVAERTS C.  
PA (PARM/) PARMENTIER M.  
PA (DETH/) DETHEUX M.  
XX  
PI Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;  
XX WPI; 2003-657983/62.  
XX P-PSDB; ADC25998, ADC26010.  
XX  
PT New human G-protein coupled receptor, useful for treating receptor-  
PT mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,  
PT acute heart failure, osteoporosis, stroke, ulcer, allergy, or  
PT neurological disorders.  
XX  
PS Claim 18; Page 14-15; 24pp; English.  
XX  
CC The invention relates to a novel G-protein coupled receptor (GPCR). The  
CC receptor, polynucleotide, agonist, reverse agonist and antagonist of the  
CC invention may be useful for treating receptor-mediated disorders  
CC including viral, fungal or bacterial infections, immune-related disorders  
CC such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,  
CC hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,  
CC ulcer and allergy, as well as psychotic and neurological disorders such  
CC as schizophrenia and dementia, degenerative diseases such as Parkinson's  
CC disease and Alzheimer's disease and dyskinesias such as Huntington's  
CC disease. The current sequence is that of the human purinergic receptor  
CC P2Y-related GPCRxl0 DNA of the invention which is located on chromosome  
CC 13.  
XX  
SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;  
Query Match 99.8%; Score 1012.4; DB 10; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 5.8e-289;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX AAD61652;  
AC 15-JAN-2004 (first entry)  
DT Human GPCRxl0 DNA.  
DE Human; G-protein coupled receptor; GPCR; infection; neoplastic process;  
XX inflammation; myocardial infarction; atherosclerosis; angina pectoris;  
KW hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;  
KW diabetes; cancer; virucide; analgesic; cardiant; gene; ds.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 1..1014  
FT /\*tag= a  
FT /product= "Human GPCR protein"  
XX US2003108986-A1.  
XX 12-JUN-2003.  
XX 20-FEB-2002; 2002US-00079384.  
XX 21-JUN-2001; 2001US-00885453.  
XX (EURO-) EUROSREEN SA.  
XX Communi D, Lannoy V, Brezillon S, Detheux M, Parmentier M;  
PI Govaerts C;  
XX WPI; 2003-810852/76.  
DR P-PSDB; ABW0808.  
XX Novel G-protein coupled receptor useful for treating viral infections,  
PT bacterial infections, fungal infections, cancer, diabetes, hypertension,  
PT osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.  
XX Claim 5; Fig 7; Opp; English.  
XX The present invention relates to novel G-protein coupled receptors  
CC (GPCRs) and the nucleic acids encoding them. The invention is useful for  
CC treating viral, bacterial and fungal infections, inflammatory and  
CC neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,  
CC angina pectoris, myocardial infarction and atherosclerosis. The present  
CC sequence is human G-protein coupled receptor (GPCR) DNA  
XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;  
SQ  
Query Match 99.8%; Score 1012.4; DB 10; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 5.8e-289;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTAATGCACTGCT 60  
Db 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTAATGCACTGCT 60  
QY 61 TTGGAATATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120  
Db 61 TTGGAATATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120  
QY 121 GGCATTATCTTCCTCGTGGGATTTCCAGCAATGCACTAGATGATACATTCATTTTC 180  
Db 121 GGCATTATCTTCCTCGTGGGATTTCCAGCAATGCACTAGATGATACATTCATTTTC 180  
QY 181 AAAATGAGACCTTTGGAAGAGCAGCACCATTATGCTGAACCTGSCCTGACAGATCTG 240  
Db 181 AAAATGAGACCTTTGGAAGAGCAGCACCATTATGCTGAACCTGSCCTGACAGATCTG 240  
QY 241 CTGTATCTGACAGCCTCCCTTCCTGATTCACCTACTATGCCAGTGGCGAAACTGGATC 300  
Db 241 CTGTATCTGACAGCCTCCCTTCCTGATTCACCTACTATGCCAGTGGCGAAACTGGATC 300  
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Db 361 ATCCTCTTCCTCAGCTGTTTCCAGCATCTCCGCTACTGTGTGATCATTCACCCAAATGAGC 420  
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Db 421 TGCCTTTCCATTCACAAAATCGATGTCAGTGTGTGATGTCGTGCTGTGATCATTT 480  
QY 481 TCACCTGTAGTGTGATTCAGTACCTTCTTGATCAGATCAACCAAGACCAACAGA 540  
Db 481 TCACCTGTAGTGTGATTCAGTACCTTCTTGATCAGATCAACCAAGACCAACAGA 540  
QY 541 TCAGCTGTCTCGACCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 541 TCAGCTGTCTCGACCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600  
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Db 601 ATTTTGATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 661 ATATTCACACTCTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db 661 ATATTCACACTCTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 721 AGGCTAACCATCTGCTACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db 721 AGGCTAACCATCTGCTACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 781 AGGTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 781 AGGTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
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Db 841 CATGAAGCTTACATGTTTCTAGACATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 CTATATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960  
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QY 961 GTACGGGACCTTTGAGCAGCAGCAAGAAATTTAGTACTCAAAAGACCCCTTGA 1014  
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RESULT 14

AAD61652

ID AAD61652 standard; DNA; 1014 BP.

QY 301 TTTGGAGATTTCATGTAAAGTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
 Db 301 TTTGGAGATTTCATGTAAAGTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
 QY 361 ATCCTCTTCTCCTCAGCTGTTTCAGCATCTTCGGCTACGTGTGTGATCATTCACCAATGAGC 420  
 Db 361 ATCCTCTTCTCCTCAGCTGTTTCAGCATCTTCGGCTACGTGTGTGATCATTCACCAATGAGC 420  
 QY 421 TGCTTTTCCATTCACAAAATCCGATGTCAGTGTGTAGCCTGTGCTGGTGTGATCATTT 480  
 Db 421 TGCTTTTCCATTCACAAAATCCGATGTCAGTGTGTAGCCTGTGCTGGTGTGATCATTT 480  
 QY 481 TCACCTGTGTCTCATTCGGATGACCTTCTTGATCAGATCAATCAACCAACAGCAACAGA 540  
 Db 481 TCACCTGTGTCTCATTCGGATGACCTTCTTGATCAGATCAATCAACCAACAGCAACAGA 540  
 QY 541 TCAGCTGTCTCAGCTCAGCTTCCAGTTCGGATGAACTCAATCAATTAAGTGTGATCACT 600  
 Db 541 TCAGCTGTCTCAGCTCAGCTTCCAGTTCGGATGAACTCAATCAATTAAGTGTGATCACT 600  
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 Db 601 ATTTGACTGCAACTACTTCTGCTCCCTCCCTGCTGATAGTACACTTTGCTATACCAAG 660  
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 Db 721 AGCTAACCATTCTGCTACTCTCTGCTTTCATTTTACGTATGTTTACCTTCCATCTTCTG 780  
 QY 781 AGGGTCATTGCGATCGAATCTCGCTGCTTTCATTCAGTGTGTTTCCATTCAGATCAGATC 840  
 Db 781 AGGGTCATTGCGATCGAATCTCGCTGCTTTCATTCAGTGTGTTTCCATTCAGATCAGATC 840  
 QY 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
 Db 841 CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900  
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 Db 901 CTATATGCTGCTGAGCAGCACTTTTCAGCAGCTGTCTGCTCAACAGTGTGATGCAAA 960  
 QY 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTAAGTTACTCAACCAACCTTGA 1014  
 Db 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTAAGTTACTCAACCAACCTTGA 1014

RESULT 15

ID ADL96473 standard; cDNA; 1014 BP.

AC ADL96473;

XX 20-MAY-2004 (first entry)

DE Human G protein-coupled receptor (GPCR) cDNA #14.

KW Human; G protein-coupled receptor; GPCR; gene; ss.

OS Homo sapiens.

PN US2003166148-A1.

PD 04-SEP-2003.

PF 16-DEC-2002; 2002US-00321807.

PR 13-OCT-1998; 98US-00170496.

XX 16-NOV-2000; 2000US-00714008.

PA (CHEN/) CHEN R.  
 PA (DANG/) DANG H T.  
 PA (LOWI/) LOWITZ K P.  
 XX

PI Chen R, Dang HT, Lowitz KP;  
 XX  
 DR WPI; 2003-898073/82.  
 DR P-PSDB; ADL96474.  
 XX

XX New G protein-coupled receptor (GPCR), useful for preparing a composition  
 PT for identifying compounds as receptors, inverse agonists or partial  
 PT agonists having potential applicability as therapeutic agents.  
 XX

PS Claim 55; SEQ ID NO 27; 82pp; English.  
 XX

CC The invention relates to G protein-coupled receptor (GPCR) polypeptides  
 CC and the polynucleotides encoding them. The GPCR polypeptides are useful  
 CC for preparing a composition for identifying compounds as receptors,  
 CC inverse agonists or partial agonists, having potential applicability as  
 CC therapeutic agents. This sequence represents human GPCR cDNA of the  
 CC invention.  
 XX

XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 11; Length 1014;  
 Best Local Similarity 99.9%; Pred. No. 5 8e-289;  
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTATAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60  
 Db 1 ATGAATGAGCCACTAGACTATTATAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60  
 QY 61 TTTGGAATGTCACATGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTAT 120  
 Db 61 TTTGGAATGTCACATGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTAT 120  
 QY 121 GGCAATTATCTTCTGCTGGGATTTCCAGGCAATGAGTAGTAGTATATCCATTTTC 180  
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Db	661	ATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGA	720
Qy	721	AGGCTAACCAATCTGCTACTCTCTGCAATTTACGATGTTTTTACCCCTTCCATATCTTG	780
Db	721	AGGCTAACCAATCTGCTACTCTCTGCAATTTACGATGTTTTTACCCCTTCCATATCTTG	780
Qy	781	AGGTCATTTCGGATCGAATCTCGCTGCTTTCAATCAGTTCGTCATTGAGAAATCAGATC	840
Db	781	AGGTCATTTCGGATCGAATCTCGCTGCTTTCAATCAGTTCGTCATTGAGAAATCAGATC	840
Qy	841	CATGAAGCTTACATCGTTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAACTGTGA	900
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Qy	901	CTATATGTGGTGGTCAGCGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA	960
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Db	961	GTAAGCGGGAACCTTTGACGAAGCAAGAAATTAGTTACTCAAAACACCTTGA	1014

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb.ba:\*

2: gb.htg:\*

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12: gb.sy:\*

13: gb.un:\*

14: gb.vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1014	100.0	1014	6	AX305130 Sequence
3	1014	100.0	1014	6	AX464561 Sequence
4	1014	100.0	1014	6	AX675828 Sequence
5	1014	100.0	1851	6	AX661905 Sequence
6	1012.4	99.8	1014	6	CQ798086 Sequence
7	1012.4	99.8	1014	6	AX148186 Sequence
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9	1012.4	99.8	1014	6	AX384211 Sequence
10	1012.4	99.8	1014	6	AX549361 Sequence
11	1012.4	99.8	1014	6	AX593341 Sequence
12	1012.4	99.8	1014	6	BD144282 Novel G-p
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14	1012.4	99.8	1014	9	AF411109 Homo sapi
15	1012.4	99.8	1029	6	AX593346 Sequence
16	1012.4	99.8	1081	6	AX458238 Sequence
17	1012.4	99.8	1092	9	AF370886 Homo sapi
18	1012.4	99.8	1179	6	AX593351 Sequence
19	1012.4	99.8	1414	6	AX646271 Sequence

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22	1012.4	99.8	2285	6	CQ843336 Sequence
23	1012.4	99.8	2285	9	AK122639 Homo sapi
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25	1012.4	99.8	67645	9	AL356486 Human DNA
26	1012.4	99.8	156555	9	AC026756 Homo sapi
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28	1010.8	99.7	1729	6	CQ493889 Sequence
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30	1010.8	99.7	1729	6	CQ498175 Sequence
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33	1009.4	99.5	1011	6	BD171271 Novel G p
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35	976.2	96.3	1020	6	AX147840 Sequence
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## ALIGNMENTS

RESULT 1	BD187507	BD187507	1014 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD187507	Novel Polypeptide.				
DEFINITION	BD187507	Novel Polypeptide.				
ACCESSION	BD187507.1	GI:32997246				
VERSION	BD187507.1	GI:32997246				
KEYWORDS	JP 2003024081-A/1.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1014)				
AUTHORS	Fidock, M.D.					
TITLE	Novel Polypeptide					
JOURNAL	Patent: JP 2003024081-A 1 28-JAN-2003;					
COMMENT	Pfizer Ltd (EP/GB) only, Pfizer Inc (US JP EP except GB)					
	OS Homo sapiens					
	PN JP 2003024081-A/1					
	PD 28-JAN-2003					
	PF 17-DEC-2001 JP 2001382712					
	PR 18-DEC-2000 GB 0030854.4, 04-MAY-2001 GB 0111031.1 PI					
	mark david fidock					
	CC					

FEATURES

source

1..1014  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

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QY	61	TTTGGAAATTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120		
Db	61	TTTGGAAATTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120		



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Db      781 AGGTCATTTCGATCGAATCTCGCTGCTTTCAATCAGTTGTTCATTCAGATCAGATC 840
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Db      901 CTATATGTGTGTGTCAGCGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAAGTCAAAA 960
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RESULT 3
AX464561
LOCUS      1014 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 1 from Patent EP1219638.
ACCESSION AX464561
VERSION    AX464561.1 GI:21899357
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Fiddock,M.D.
TITLE      G-protein coupled receptors having homology to the p2y
JOURNAL    Patent: EP 1219638-A 1 03-JUL-2002;
Pfizer Limited (GB) ; Pfizer Inc. (US)
FEATURES   Location/Qualifiers
source     1..1014
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Best Local Similarity 100.0%; Pred. No. 2.8e-257;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      421 TGCTTTTCCATTACAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTGGATCAT 480
Qy      481 TCAGTGTAGTGTTCATTCGGATGACCTTTTGTATCATCAACCAACAGGACCAACAGA 540
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Qy      901 CTATATGTGTGTGTCAGCGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTGAAGTCAAAA 960
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Qy      961 GTAAGCGGGAACCTTGAGCAAGCAAGAAAGAAATAGTTACTCAAAACACCCCTTGA 1014
Db      961 GTAAGCGGGAACCTTGAGCAAGCAAGAAAGAAATAGTTACTCAAAACACCCCTTGA 1014

RESULT 4
AX675828
LOCUS      1560 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 5 from Patent WO02057452.
ACCESSION AX675828
VERSION    AX675828.1 GI:29333662
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shinkets,R.A., Colman,S.D., Spytek,K.A., Ballinger,R.A., Guo,X.,
Tchernev,V.T., Shenoy,S.G., Li,L., Ellerman,K.E., Zerhusen,B.D.,
Patturajan,M., Casman,S.J., Boldog,F., Gusev,V.Y., Burgess,C.E.,
Edinger,S., Gangolli,E.A., Malyankar,U.M., Gunther,B., Smithson,G.,
Millett,I. and Gerlach,V.L.
TITLE      Human proteins, polynucleotides encoding them and methods of using
            the same
JOURNAL    Patent: WO 02057452-A 5 25-JUL-2002;
Curagen Corporation (US)
FEATURES   Location/Qualifiers
source     1..1560
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            /db_xref="taxon:9606"

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Query Match      100.0%; Score 1014; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 2.9e-257;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 653 TTTGAGATTTTCATGTGAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGCAGC 712  
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RESULT 5  
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LOCUS AX661905 1851 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 7 from Patent WO02055702.  
ACCESSION AX661905

AX661905.1 GI:29162960  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE  
AUTHORS Gangoli, E.A., Spytek, K.A., Gilbert, J., Casman, S., Blalock, A.,  
Li, L., Vernet, C.A., Shenoy, S., Mishra, V., Furtak, K., Gerlach, V.,  
Edinger, S., Malvankar, U., Stone, D., Millet, I., Smithson, G.,  
Gunther, E., Padigaru, M., Taupier, R.J., and Anderson, D.  
TITLE Human proteins, polynucleotides encoding them and methods of using  
the same  
JOURNAL Patent: WO 02055702-A 7 18-JUL-2002;  
Curagen Corporation (US)  
FEATURES  
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Query Match 100.0%; Score 1014; DB 6; Length 1851;  
Best Local Similarity 100.0%; Pred. No. 2.9e-257;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 587 CTGATCTGACAGCTCCCTTCCTGATTCATCTACTACTATGCCAGTGGCGAAACTGGATC 646  
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Db 707 ATCCCTCTCTCCTCCTGTTTACGATCTTCGCTACTGCTGATCAATTCACCAATGAGC 766  
Qy 421 TGCCTTTCCATTCACAAACTCGATGTCAGTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 767 TGCCTTTCCATTCACAAACTCGATGTCAGTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 826  
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Db |||||
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Db |||||
QY 1127 AGGCTATCTGGATCGAATCTCGCTGCTTTCATATGTTTTCATATGTTTTCATATCTTG 1186
Db |||||
QY 841 CATGAAGCTTACATCTGTTTCTAGACCAATAGCTGCTCTGACACCTTTGTTAACTCTGTTA 900
Db |||||
QY 1187 CATGAAGCTTACATCTGTTTCTAGACCAATAGCTGCTCTGACACCTTTGTTAACTCTGTTA 1246
Db |||||
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Db |||||
QY 1247 CTATATGTGTGTGCTAGCGCAAACTTTTCAGCAGGCTGCTGCTCAACAGTGAGATGCAAA 1306
Db |||||
QY 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAGTTTACTCAAAACACCTTGA 1014
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QY 1307 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAGTTTACTCAAAACACCTTGA 1360
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RESULT 6
LOCUS CQ798086 1014 bp DNA linear PAT 20-APR-2004
DEFINITION Sequence 1 from Patent WO2004029626.
ACCESSION CQ798086
VERSION CQ798086.1 GI:46426507
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Inbe.H. and Encinas,J.
TITLE Regulation of human p2y15 g protein-coupled receptor
JOURNAL Patent: WO 2004029626-A 1 08-APR-2004;
Bayer HealthCare AG (DE)
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## ORIGIN

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Query Match 99.8%; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db |||||
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Db |||||
QY 301 TTTGGAGATTTCTATGTGTAAAGTTTATTCGGTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
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QY 361 ATCCTCTTCTCAGCTGTTTTCAGCATCTTCGCTACTGTGTGATCATTTCAACCTGATGAGC 420
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QY 421 TGTCTTTTCCATTCACAAACTCGATGTGCAAGTTGTAGCCTGTGTGTGTGTGATCATTT 480
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QY 481 TCACTGTGTAGTGTCTCATTTCCGATGACCTTCTTGCATCAGATCAACCAACAGCAACAGCA 540
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RESULT 7
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DEFINITION Sequence 27 from Patent WO0136471.
ACCESSION AX148186
VERSION AX148186.1 GI:14347086
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,R., Dang,H.T. and Lowitz,K.P.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
receptors
JOURNAL Patent: WO 0136471-A 27 25-MAY-2001;
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QY 541 TCAGCCTGTCTCGACCTCACAGTTCCGATGCAACTCAATATTAAGTGGTACAACTTA 600
Db 541 TCAGCCTGTCTCGACCTCACAGTTCCGATGCAACTCAATATTAAGTGGTACAACTTA 600
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Db 961 GTAAAGCGGGAACCTTGAGCAAGCAAGAAATAGTTTACTCAAAACCCCTTGA 1014

RESULT 9
AX384211
LOCUS AX384211 1014 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 5 from Patent WO214511.
ACCESSION AX384211
VERSION AX384211.1 GI:19577652
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Ramakrishnan,S.
JOURNAL Regulation of human p2y1-like G protein-coupled receptor
Bayer Aktiengesellschaft (DE)
FEATURES
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGAATTATGAGCTGCT 60
Db 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGAATTATGAGCTGCT 60
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RESULT 10
AX549361
LOCUS AX549361 1014 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 646 from Patent WO02061087.
ACCESSION AX549361
VERSION AX549361.1 GI:25813991
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Burner,G.C., Roush,C.L. and Brown,J.P.
JOURNAL Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 646 08-AUG-2002;
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Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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FEATURES
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    Query Match      99.8%; Score 1012.4; DB 6; Length 1014;
    Best Local Similarity 99.9%; Pred. No. 7.4e-257;
    Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTCTGATTTCCCGGATTTATGACGCTGCT 60
DB 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTCTGATTTCCCGGATTTATGACGCTGCT 60
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DB 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCATCTCCCTGCTTTATTTAT 120
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DB 121 GGCATTATCTCTCGTGGGATTTCCAGCAATGCAATGATGATATCCACTTTACATTTTC 180
QY 181 AAAATGAGACCTTGGAAAGAGCAGCACCATCATTTAGTGAACCTGGCCCTGCACAGATCTG 240
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DB 241 CTGATATCTGACGAGCTCCCTCTCTGATTTCACTACTATGCGAGTGGGGAACCTGGATC 300
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RESULTS
AX593341
LOCUS AX593341 1014 bp DNA linear PAT 13-FEB-2003
DEFINITION Sequence 2 from Patent WO0208183.
ACCESSION AX593341
VERSION AX593341.1 GI:28374719
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Carlton, M., Aparicio, S., Dixon, J. and Hendrick, A.
TITLE Receptor
JOURNAL Patent: WO 0208183-A 2 07-NOV-2002;
Paradigm Therapeutics Limited (GB)
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    Best Local Similarity 99.9%; Pred. No. 7.4e-257;
    Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 12  
BD144282  
LOCUS  
DEFINITION  
Novel G-protein coupled receptors.  
ACCESSION  
BD144282  
VERSION  
BD144282.1 GI:27850040  
KEYWORDS  
JP 2002112793-A/7.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS  
Haga, T., Takeda, S. and Miyake, N.  
TITLE  
Novel G-protein coupled receptors  
JOURNAL  
Patent: JP 2002112793-A 7 16-APR-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002112793-A/7  
PD 16-APR-2002  
PF 09-FEB-2001 JP 2001034434  
PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE  
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C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K45/00, PC  
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PC A61P43/00, C07K14/705, C07K16/28, C07K19/00, C12N1/15, C12N1/19, PC  
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PC C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC  
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PC C12P21/08, C12N15/00, A61K37/02, C12N5/00  
CC Novel G-protein coupled receptors  
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ORIGIN

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 7.4e-257;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13  
AB083598  
LOCUS

AB083598 1014 bp DNA linear PRI 24-MAY-2002

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DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor, complete CDS, clone:hGPCR16.

ACCESSION AB083598

VERSION AB083598.1 GI:20152259

KEYWORDS

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Takeda, S., Kadowaki, S., Haga, T., Takesue, H. and Mitaku, S.

TITLE Identification of G protein-coupled receptor genes from the human genome sequence

JOURNAL Unpublished

AUTHORS Takeda, S., Kadowaki, S., Haga, T., Takesue, H. and Mitaku, S.

TITLE Direct Submission

JOURNAL Department of Biological and Chemical, Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan

(E-mail:stakeda@bce.gunma-u.ac.jp, Tel:++81-277-30-1434, Fax:++81-277-30-1434)

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;

Best Local Similarity 99.9%; Pred. No. 7.4e-257;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGCGCTGCT 60

QY 61 TTGGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTAT 120

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AF411109 1014 bp DNA linear PRI 01-NOV-2001

DEFINITION Homo sapiens G protein-coupled receptor (GPR80) gene, complete cds.

ACCESSION AF411109

VERSION AF411109.1 GI:16566322

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1014)

AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

TITLE Discovery and mapping of ten novel G protein-coupled receptor genes

JOURNAL Gene 275 (1), 83-91 (2001)

MEDLINE 21458557

PUBMED 11574155

REFERENCE 2 (bases 1 to 1014)

AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

TITLE Direct Submission

JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. 4953, Toronto, Ont M5S 1A8, Canada

FEATURES

Location/Qualifiers

1..1014

/organism="Homo sapiens"

source







GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Maximum Match 100%  
Listing first 45 summaries

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4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	735.6	72.5	1014	9	AY404081 Mus muscu
4	381.6	37.6	870	9	CC579146
5	243	24.0	744	4	BM723768
6	189.6	18.7	800	7	CN511791
7	185.8	18.3	725	6	CA385979
8	175.4	17.3	681	6	CA384807
9	155.4	15.3	3613	3	AK030759
10	153.8	15.2	1122	9	AY413141
11	153.8	15.2	2203	3	AK033660
12	153.8	15.2	3888	3	AK036611
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14	147.8	14.6	781	6	CF284315
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
Homo sapiens GPR80 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY404079  
VERSION  
AY404079.1  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1014)  
AUTHORS  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL  
Science 302 (5652), 1960-1963 (2003)  
PUBMED  
14671302  
REFERENCE  
2 (bases 1 to 1014)  
AUTHORS  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1. 1014  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<!--1014  
/gene="GPR80"  
/locus\_tag="HCM1771"

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 7.6e-281;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGCATTTACAGCTGCT 60  
|||||

Db 1 ATGAATGAGCAGCTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGCAAGTCT 60  
Qy 61 TTTTGGAAATTCAGTATGAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
Db 61 TTTTGGAAATTCAGTATGAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
Qy 121 GGCATTATCTTCCCTGCTGGGATTTCCAGGCAATGCACTAGTATGATCCACTTACATTTTC 180  
Db 121 GGCATTATCTTCCCTGCTGGGATTTCCAGGCAATGCACTAGTATGATCCACTTACATTTTC 180  
Qy 181 AAAATGAGACTTGGAG 240  
Db 181 AAAATGAGACTTGGAG 240  
Qy 241 CTGTATCTGACGAGCTCCCTTCTGATTCACATCACTATGCACTGAGTGGGAGAACTGGATC 300  
Db 241 CTGTATCTGACGAGCTCCCTTCTGATTCACATCACTATGCACTGAGTGGGAGAACTGGATC 300  
Qy 301 TTTTGGAGATTTTCACTGTATGATTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Db 301 TTTTGGAGATTTTCACTGTATGATTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360  
Qy 361 ATCTCTTCTCACTGTTTTCAGAGATCTTCGCTACTGCTGTATGATCACTTCAACCTATGAGC 420  
Db 361 ATCTCTTCTCACTGTTTTCAGAGATCTTCGCTACTGCTGTATGATCACTTCAACCTATGAGC 420  
Qy 421 TGCTTTTCCATTCACAAACTCGATGTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 421 TGCTTTTCCATTCACAAACTCGATGTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Qy 481 TCACCTGTAGTGTCTTCCGATGACCTTCTTGTATCAATCAACCAAGAGAGAGAGAGAGAG 540  
Db 481 TCACCTGTAGTGTCTTCCGATGACCTTCTTGTATCAATCAACCAAGAGAGAGAGAGAGAG 540  
Qy 541 TCAGCTGTCTGACCTTCAACAGTTCGATGAAGAACTCAATATATTAAGTGGTGAACCTTA 600  
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Qy 601 ATTTTGTAGTGAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 ATTTTGTAGTGAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Qy 661 ATTTTGTAGTGAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
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Qy 721 AGGCTAACCATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
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Qy 781 AGGCTAACCATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Db 781 AGGCTAACCATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 841 CATGAAGCTTACATGCTTCTAGACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 CATGAAGCTTACATGCTTCTAGACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Db 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Qy 961 GTAAGCGGAACTTTGAGCAAGCAAGAAATTTAGTACTCAAAACCCCTTGA 1014  
Db 961 GTAAGCGGAACTTTGAGCAAGCAAGAAATTTAGTACTCAAAACCCCTTGA 1014

RESULT 2  
AY404080  
LOCUS Pan troglodytes GPR80 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY404080

VERSION AY404080.1 GI:39760063  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE 1 (bases 1 to 1005)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1005)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1005  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
gene  
1..1005  
/gene="GPR80"  
/locus\_tag="HCM1771"  
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Query Match 93.2%; Score 944.6; DB 9; Length 1005;  
Best Local Similarity 94.2%; Pred. No. 2.9e-261;  
Matches 947; Conservative 0; Mismatches 58; Indels 0; Gaps 0;  
Qy 10 CCACCTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGCAAGTCTGCTTTTGGAAAT 69  
Db 1 CCACCTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGCAAGTCTGCTTTTGGAAAT 60  
Qy 70 TGCACCTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTATGCGCATATTC 129  
Db 61 TGCACCTGATGAAACATCCCACTCAAGATGNNCTACCTCCCTNNNATCTATGCGCATATTC 120  
Qy 130 TTCTCTGCGGATTTCCAGGCAATGCACTAGTATGATTCACCTTACATTTTCAAAATGAGA 189  
Db 121 TTCTCTGCGGATTTCCAGGCAATGNNNGTGGATATCCACTTACATTTTCAAAATGAGA 180  
Qy 190 CTTTGGAAAGAGCAGCACCACCATCATTTATGCTGAACCTGGCTGCGCAGATCTGCTGATCTG 249  
Db 181 CTTTGGAAAGAGCAGCACCACCATCATTTATGCTGAACCTGGCTGCGCAGATCTGCTGATCTG 240  
Qy 250 ACCAGCTCCCTTCTGATTCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309  
Db 241 ACCAGCTCCCTTCTGATTCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Qy 310 TTCTGCTGATTTTATCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 369  
Db 301 TTCTGCTGATTTTATCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 360  
Qy 370 CTCACCTGTTTCCAGCATCTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429  
Db 361 CTCACCTGTTTCCAGCATCTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Qy 430 ATTCAAAAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489  
Db 421 ATTCAAAAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Qy 490 GCTGCTTCCGATGACCTTCTGATCATCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549



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Db      961 GCACGGGGGACCTTGACAAAGAAAGAAAGACAGTTGCTCAACACACCCTTGA 1014

RESULT 4
CC579146      870 bp      DNA      linear      GSS 18-JUN-2003
LOCUS      CH240_458M22.T7 CHORI-240 Bos taurus genomic clone CH240_458M22,
DEFINITION      genomic survey sequence.
ACCESSION      CC579146
VERSION      CC579146.1 GI:31924524
KEYWORDS      GSS.
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
REFERENCE      1 (bases 1 to 870)
AUTHORS      Holt,R., Stott,J., Yang,G., Barber,S., Smalrus,D., Prabhu,A.-L.,
      Tsai,M., Cloutier,A., Lee,D., Girm,N., Olson,T., Mayo,M.,
      Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
      Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
      Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
      Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
      Unpublished (2003)
      Other GSSs: CH240_458M22.TARBAC13P2
      Contact: Rob Holt
      Sequencing
      The British Columbia Cancer Agency Genome Science Centre
      600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
      Tel: 604-877-6085
      Fax: 604-877-6276
      Email: rholt@bcgsc.ca
      Clones are derived from the bovine BAC library CHORI-240
      (http://www.chori.org/bacpac/bovine240.htm). For BAC library
      availability, please contact Pieter de Jong (pjejong@mail.cho.org).
      Clones may be purchased from BACPAC Resources
      (http://www.chori.org/bacpac/ordering/information.htm). This work
      was undertaken as part of the International Bovine BAC Mapping
      Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
      British Columbia Genome Sciences Centre, Canada.
      Plate: 458 row: M column: 22
      Seq primer: T7
      Class: BAC ends.
      Location/Qualifiers
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          /organism="Bos taurus"
          /mol_type="genomic DNA"
          /strain="bred: Hereford"
          /db_xref="taxon:9913"
          /clone="CH240_458M22"
          /sex="Male"
          /cell_type="Blood"
          /clone_lib="CHORI-240"
          /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
      Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
      library (Male) produced by Pieter de Jong"

FEATURES
      source
      Query Match      37.6%; Score 381.6; DB 9; Length 870;
      Best Local Similarity      84.8%; Pred. No. 1.3e-98;
      Matches 451; Conservative 0; Mismatches 79; Indels 2; Gaps 2;

Oy      1 ATGAATGAGCCACTAGACTATTAGCAATAGTTCTGATTTCCCGAATTATG-CAGCTGC 59
      Db      339 ATGAATGAGCCACTAGACTATTGCAATGCTCTGATTTCCCTGATTATGTCAGCTGC 398
      Oy      60 TTTTGGAAATTCATCGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTA 119
      Db      399 TCTTGAAATTCACCAAGTGAATAATCCCACTCAAGAGCGCACTACCTCCCTGTTATTTA 458
      Oy      120 TGGCATTA-TCTTCTCCGCGGATTTCCAGGCAATGCAGTACTGATATCCACTTACATTT 178
      Db      459 TAGCATCATCTCTCTCTGGGGTTTCTCGGAATGTGATAGCCATCTCCACATCACT 518

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Oy      179 TCAAAATGAGACCTTGGAGAGCAGACCAATCAATTAATGCTGAACCTGGCCTGCACAGATC 238
      Db      519 TCAAAATGGGCGCTGGAGAGCAGACCAATCAATCAATGCTGAACCTGGCCTGCACCGACC 578
      Oy      239 TGCTGATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGGAAACCTGGA 298
      Db      579 TGCTGATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGGCGGAGACCACTGGG 638
      Oy      299 TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA 358
      Db      639 TCTTCGGGAGCTCACTGTCAGTTTATCCGCTTCGCTTCCACTTCAACCTGTATAGCA 698
      Oy      359 GCATCTCTTCTTCACCTGTTTCAGCATCTTCGCTACTGCTGATCAATTCACCAATGA 418
      Db      699 GCATCTCTTCTTCACCTGTTTCAGCATCTTCGCTACTTTCGCTACTTTCATTCACCCACGA 758
      Oy      419 CTGCTTTTTCATTCACAAACCTCGATGTCAGTTGCTGAGCTGTGCTGTGTGGATCA 478
      Db      759 GCTGCTTCTCGTCCACAAAAGCGATGGGCGCATGGTGGCTGTGTGTGTGGATCG 818
      Oy      479 TTTCACTGTGAGTGTGTCATTTCCGATGACCTTCTTTGATCAGATCAACCAACAG 530
      Db      819 TGTGCTGTGGCGTATACCATGACCTTCTGATCAGACTACCACTACCAACAG 870

RESULT 5
BM723768      744 bp      mRNA      linear      EST 01-MAR-2002
LOCUS      UI-E-E01-aix-g-16-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone
DEFINITION      UI-E-E01-aix-g-16-0-UI 5', mRNA sequence.
ACCESSION      BM723768
VERSION      BM723768.1 GI:19045099
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 744)
AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
      Normalization and subtraction: two approaches to facilitate gene
      discovery
      Genome Res. 6 (9), 791-806 (1996)
      97044477
      8889548
      Contact: Soares, MB
      Coordinated Laboratory for Computational Genomics
      University of Iowa
      375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
      Tel: 319 335 8250
      Fax: 319 335 9565
      Email: bento-soares@uiowa.edu
      Tissue Procurement: Dr. Gregg Hageman
      cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
      cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: Researchers may obtain clones from Research
      Genetics (www.resgen.com).
      Seq primer: M13 Reverse.
      Location/Qualifiers
        1..744
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          /mol_type="mRNA"
          /db_xref="taxon:9606"
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          /tissue_type="fetal eye"
          /dev_stage="fetal"
          /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
          /clone_lib="UI-E-E01"
          /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
      modified polylinker; Site 1: EcoR I; Site 2: Not I;
      UI-E-E01 is a normalized cDNA library containing the
      following tissue(s): fetal eye. The library was

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constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCGGATATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 24.0%; Score 243; DB 4; Length 744;  
Best Local Similarity 100.0%; Pred. No. 1.4e-58; Indels 0; Gaps 0;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 772 CATATCTTTGAGGTCATTGGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTGAG 831  
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1 CATATCTTTGAGGTCATTGGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTGAG 60  
QY 832 AATCAGATCCATGAAGCTTACATGCTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGT 891  
Db |||||  
61 AATCAGATCCATGAAGCTTACATGCTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGT 120  
QY 892 AACCTGTTACTATATGTTGGTGTGAGGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTG 951  
Db |||||  
121 AACCTGTTACTATATGTTGGTGTGAGGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTG 180  
QY 952 AGATCAAGTAAGCGGAACTCTGAGCAAGCAAGAAATTTAGTTACTCAACAAACCTT 1011  
Db |||||  
181 AGATCAAGTAAGCGGAACTCTGAGCAAGCAAGAAATTTAGTTACTCAACAAACCTT 240  
QY 1012 TGA 1014  
Db |||||  
241 TGA 243

RESULT 6

CNS11791  
LOCUS AGENCOURT\_22438125 NIH\_ZGC\_7 Danio rerio cDNA clone IMAGE:7269123  
DEFINITION 5', mRNA sequence.  
ACCESSION CNS11791  
VERSION CNS11791.1 GI:46824415  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 800)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabp-r@mail.nih.gov](mailto:cgabp-r@mail.nih.gov)  
Tissue Procurement: Len Zon, Harvard  
cDNA Library Preparation: Open Biosystems  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILLNL at:  
<http://image.llnl.gov>  
plate: LHAM15249 row: j column: 01  
High quality sequence stop: 713.  
Location/Qualifiers  
1..800  
/organism="Danio rerio"

FEATURES  
source

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/clone=IMAGE:7269123"  
/tissue\_type="whole body"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_ZGC\_7"  
/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;  
Bulk tissue was collected from a whole adult individual  
from the Tuebingen strain. 1st strand cDNA was primed with  
a Not I - oligo(dT) primer, double-stranded cDNA was  
cloned into the Not I and EcoRV sites of pExpress-1.  
Library was size-selected for >1 kb fragments and  
normalized. A non-normalized version of this library is  
also available (NIH\_ZGC10). Library was constructed by  
Open Biosystems (Huntsville, AL)"

ORIGIN

Query Match 18.7%; Score 189.6; DB 7; Length 800;  
Best Local Similarity 54.6%; Pred. No. 3.7e-43;  
Matches 400; Conservative 0; Mismatches 330; Indels 3; Gaps 1;  
QY 57 TGCCTTTTGGAAATTCGACTGATGAAAAATCCCACTCAAGATGCACCTACTCCCTGTAT 116  
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70 TCTCTTTGGACAACTCGACCGATGTGGACGACAAAGGTGAAGCGCTACTATCTGCCAGCCAT 129  
QY 117 TTATGGCATATCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACAT 176  
Db |||||  
130 GTAAGTGGCATCTTCTCATAGTGGGTGATTTGGAACAATCACAGCTCTTCTGGTGTATCT 189  
QY 177 TTTCAAAATGAGACCTTTGGAAGAGCAGCACCACCATCATTTATGCTGAACTGGCCTGCACAGA 236  
Db |||||  
190 GCTCAAGGTTGACCTCGAAGAGAGCAGCACCACCATCATCTGTTGAACCTGGTCTCACAGA 249  
QY 237 TCTGCTGTATCTGACAGCCTCCCTTCTCGATTCACCTACTATGCGAGTGGCGAAACATG 296  
Db |||||  
250 TCTCCTCTTCATGATCTCGCTGCCATTTTATAGTGTATTACTATGTGTGCAATGATCGTG 309  
QY 297 GATCTTTGGAGATTCATGTGTAGTTTATCGCTTCAGCTTCCATTTCAACCTGTATAG 356  
Db |||||  
310 GACTCTGGAAATCACCGTGTGCTGCGCTTCGCGCTTCATCTTCCACTTCAACCTGTACGG 369  
QY 357 CAGCATCTCTTCTCCTCAGCTGTTTCAGCATCTTCCGCTACTCTGTGATCATCAACCAACGAGCA 416  
Db |||||  
370 CAGCATCTCTTCTCCTCAGATGCTTCTCATTTTTCGCTATGTAGCAATCGTGATCCGCA 429  
QY 417 GAGCTGCTTTTCCATTCACAAACTCTGATGTCAGTTGTAGCCTGTGCTGTGGTGTGGAT 476  
Db |||||  
430 GCACCTCACAAAGATTTCGGCGCAACGCTGGGGCGTTGTATCTTGTGGCTGTGGT 489  
QY 477 CATTTTCAGTGTGTGTCATTCGATGACCTCTTCTGATCATCATCAACCAACGAGCA 536  
Db |||||  
490 TGTACAGTGGCTGAACCTGAGTGCACATTTTAACTGTTTTCGCGATGGAGATCGATAA 549  
QY 537 CAGATCAGCTGTCTCGACCTCAGCAGTTCGAGTGAACCTCAATCTATTAAGTGTGTACAA 596  
Db |||||  
550 CAAACATCTGTTGGATTTTGGAGCAATGATGCTC---AAAAGATTTGGCGGTATAG 606  
QY 597 CCTAATTTTGTGCAACTACTTTCTGCTCCCTTGGGTGTAGTGTGATGACACTTTTGTCTATAC 656  
Db |||||  
607 TTGGGTGTGACAGTACTTGGCTATTTAGTTCTCTTGTAGTGGTGTCTGTGTCTGTATTG 666  
QY 657 CACGATTTCCACTCTGACCCCTGACCACTGCAAACTGACAGCTGCCTTAAAGCAGAAAGC 716  
Db |||||  
667 GCGCATCATCAAGAGCTAAAGAGGGGTCTCATATGGGGGTGCNAAAACAGTGCAGC 726  
QY 717 ACGAAGGTAACCACTTCTGCTACTCTTCTGATTTTACGTATGTTTTCCTTCCATAT 776  
Db |||||  
727 GAGGAGATTCATTGTGCTCATTTTTCAGCTGTTTTCGGGTGTTTCTTCTCGTTCACT 786  
QY 777 CTTGAGGCTCAT 789  
Db |||||  
787 GCTGCGAGCGTT 799





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Matches 296; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
QY 67 AATGCACTGATGAAGACATCCCACTCAAGATCACTACCTCCCTGTTATTTATGCAATT 126
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
111 AACTGCACCAATGTGACACCCCTGATGAACGCTACTACTGCGCCGTCATGACACATA 170
QY 127 ATCTTCTCTGTTGGATTTCCAGCAATGACAGTAGTGATATCCACTTTTCAAAATG 186
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
171 ATTTCTGTTGTTGGGCTGTTGGTAACTGACCTCCATCGCCATCTACCTGATCAAGCTA 230
QY 187 AGACCTTGAAGAGCAGCACCATTATGCTGAACCTGCGCTGCACAGATCTGCTGTA 246
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
231 CGACCTGGAAGTCCAGCAGTATCATATGTTCAACTGCGCTGACGAGTCTTCTGTAT 290
QY 247 CTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATCTTTGA 306
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
291 GTTCTGAGTCTGCTTTGATGTTACTACTACTACCAACGGTGAATCTTGACCTGGCG 350
QY 307 GATTTCATGTTAAGTTTATCGCTTCAGCTTCCATTTCAACTGATAGCAGATCCTC 366
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 GACTTCATGCGTCTGCTTTCTGCGTTTCTGCGTTTCCACTTTAACTATATGATGATCTG 410
QY 367 TTCTTCACCTGTTTCAAGCATCTTCGCTACTGTCGATCATTCACCAATGAGCTGCTT 426
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
411 TTCTTCACCTGTTTCTGCTGTTTCTGATATGTCGCGCGCATCTCTGAGGGCGCG 470
QY 427 TCATTCACAAACTCGATGTCAGTGTGAGCTGTGCTGTGTGTGATCATTTTCACTG 486
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
471 CAGGTGTCAGCAGAGGAGTGGGTATCTTGGCGTGTGCTGTGTGCTGGCCATAGCTGTG 530
QY 487 GTAGCTGTATTCCTGATGACCTTCTTGTATCATATCAACCAAGGACCAAGATCAGCC 546
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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ACCESSION AK030759
VERSION AK030759.1 GI:26326762
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Mech. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12053091
6 (bases 1 to 3613)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
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Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1122)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1122)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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VERSION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1122)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
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Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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 Unpublished (1999)  
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 COMMENT  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics

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National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-x@mail.nih.gov  
 Tissue Procurement: Dr. Igor Dawid  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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 /dev\_stage="adult"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NICHD XGC Spl"  
 /note="Organ: spleen; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 2.4 kb. Constructed by Life  
 Technologies."

## ORIGIN

Query Match 14.6%; Score 147.8; DB 6; Length 781;  
 Best Local Similarity 56.7%; Pred. No. 4.4e-31;  
 Matches 272; Conservative 0; Mismatches 208; Indels 0; Gaps 0;  
 QY 66 AAATGGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTATGGCAT 125  
 Db |||||  
 QY 257 AAAATGCTCTCTGCAAAAGACAGGCTTTTCAGTTCTATTACCTCCCTCGCTATATAGT 316  
 Db |||||  
 QY 126 TATCTTCTCTGGGATTTCCAGCAATGCAAGTAGTAGTATCCACTTACATTTTCAAAT 185  
 Db |||||  
 QY 317 CGTCTGCATCAGGGATTCATGGGAAACAGTGTGGCCATATGGATGTTTCATTTTCATAT 376  
 Db |||||  
 QY 186 GAGACCTTGGAAAGACGACGACCATCATTTATGCTGAACCTGGCTGCACAGATCTCTGTA 245  
 Db |||||  
 QY 377 GAAACCATGGAGCAGTATCTCGTCTATATGTTTAACTGGCTTAGCGGATTTCTTTA 436  
 Db |||||  
 QY 246 TGTGACAGCTCTCCCTTCTGATTTCACTACTATGCCAGTGGCGAAACTGGATCTTTGG 305  
 Db |||||  
 QY 437 TGTCTGTCTCTCCCGGCTGATATTTTATTTTCAATAAAGACAGCTGGATCTTTGG 496  
 Db |||||  
 QY 306 AGATTTTCATGTTAAGTTTATCCGCTTCAGCTTCCATTTCCACTTCAACCTGTATAGCAGTCT 365  
 Db |||||  
 QY 497 GGATGCCCTTGTGCAAACTACAAACGCTTTATTTTCCATGTTAATCTTTATGGCAGCATCT 556  
 Db |||||  
 QY 366 CTTCTCTACCTGTTTTCAGCATCTCCGCTACTGTGTGATCAATTCACCAATGAGCTGCTT 425  
 Db |||||  
 QY 557 GTTCTTGACTGATCAGCGTGCACGTTTACAGGGTTGTACATCCACTTAAGTCACT 616  
 Db |||||  
 QY 426 TTCCATTCACAAACTCGATGTGAGTGTAGCTGTGCTGTGGTGGATCAATTTCACT 485  
 Db |||||  
 QY 617 TGGGAGGCTGGAAGAAGAAATTCATCTACATGACCTGGTCTGGTCTCATTTGTCAT 676  
 Db |||||  
 QY 486 GGTAGCTGTCTTCGATGACCTTCTGTATCACAATCAACCAAGACGACCAACAGATCAGC 545  
 Db |||||  
 QY 677 AGCCGGTATTTCTCCCATCCTTTTCTTCTCGGAGCTGSCATCANGAAAAACAACCATC 736  
 Db |||||

RESULT 15  
 CA367446  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 Xenopus laevis (rainbow trout)

CA367446  
 643337 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT109D02\_D\_B01  
 5', mRNA sequence.

CA367446  
 CA367446  
 CA367446.1 GI:24678523  
 EST.

Oncorhynchus mykiss (rainbow trout)





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**This Page blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 14:50:30 ; Search time 43 seconds  
(without alignments)  
754.071 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFDYAAA.....RCKVSGNLEQAKKISVSNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 567   | 32.0        | 373    | 2  | JC4737             |
| 2          | 565.5 | 31.9        | 362    | 2  | G protein-coupled  |
| 3          | 562   | 31.7        | 373    | 2  | P2Y1 receptor - bo |
| 4          | 514   | 25.0        | 365    | 2  | G protein-coupled  |
| 5          | 479   | 27.0        | 373    | 2  | ATP receptor P2u - |
| 6          | 438   | 24.7        | 373    | 2  | P-2U nucleotide re |
| 7          | 423   | 23.9        | 328    | 2  | G protein-coupled  |
| 8          | 419.5 | 23.7        | 420    | 2  | thrombin receptor  |
| 9          | 405   | 22.9        | 328    | 2  | P2Y6 receptor - hu |
| 10         | 397   | 22.4        | 427    | 2  | alpha-thrombin rec |
| 11         | 396.5 | 22.4        | 432    | 2  | thrombin receptor  |
| 12         | 388.5 | 21.9        | 399    | 2  | proteinase activat |
| 13         | 388.5 | 21.9        | 425    | 2  | thrombin receptor  |
| 14         | 380   | 21.5        | 308    | 2  | G protein-coupled  |
| 15         | 376.5 | 21.3        | 361    | 2  | G protein-coupled  |
| 16         | 376.5 | 21.3        | 397    | 2  | G protein-coupled  |
| 17         | 370   | 20.9        | 355    | 2  | proteinase-activat |
| 18         | 356   | 20.1        | 383    | 2  | chemokine (C-C) re |
| 19         | 355   | 20.0        | 352    | 2  | G protein-coupled  |
| 20         | 354   | 20.0        | 352    | 2  | fusin (LESTRA) - c |
| 21         | 353   | 19.9        | 362    | 2  | neuropeptide Y/pep |
| 22         | 353   | 19.9        | 362    | 2  | G protein-coupled  |
| 23         | 349.5 | 19.7        | 423    | 2  | G protein-coupled  |
| 24         | 349   | 19.7        | 356    | 2  | allotostatin recep |
| 25         | 348   | 19.6        | 354    | 2  | interleukin-8 rece |
| 26         | 348   | 19.6        | 362    | 2  | G protein-coupled  |
| 27         | 347.5 | 19.6        | 363    | 2  | G protein-coupled  |
| 28         | 346.5 | 19.6        | 344    | 2  | angiotensin II rec |
| 29         | 345.5 | 19.5        | 363    | 2  | intron 17 purinerg |
|            |       |             |        |    | angiotensin II rec |

|    |       |      |     |   |        |
|----|-------|------|-----|---|--------|
| 30 | 344.5 | 19.5 | 378 | 2 | B55735 |
| 31 | 344   | 19.4 | 353 | 2 | JC2492 |
| 32 | 340   | 19.2 | 370 | 2 | JC2549 |
| 33 | 339.5 | 19.2 | 363 | 2 | JC2543 |
| 34 | 339   | 19.1 | 360 | 2 | G02064 |
| 35 | 338.5 | 19.1 | 359 | 2 | S15403 |
| 36 | 337   | 19.0 | 353 | 2 | S28787 |
| 37 | 336.5 | 19.0 | 360 | 2 | A53611 |
| 38 | 336   | 19.0 | 362 | 2 | JN0694 |
| 39 | 334   | 18.9 | 356 | 2 | I49340 |
| 40 | 332.5 | 18.8 | 355 | 2 | JQ1231 |
| 41 | 328   | 18.5 | 355 | 2 | A45177 |
| 42 | 327   | 18.5 | 355 | 2 | JC5067 |
| 43 | 327   | 18.5 | 387 | 2 | I62022 |
| 44 | 326.5 | 18.4 | 378 | 2 | A45680 |
| 45 | 325.5 | 18.4 | 359 | 2 | I39418 |

## ALIGNMENTS

### RESULT 1

JC4737

G protein-coupled receptor P2Y1 - human

N/Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C/Species: Homo sapiens (man)

C/Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C/Accession: JC4737; JC4615; S54253

R/Janssens, R.; Communi, D.; Piroton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A/Title: Cloning and tissue distribution of the human P2Y1 receptor.

A/Reference number: JC4737; MUID:96205320; PMID:8630005

A/Accession: JC4737

A/Molecule type: DNA

A/Residues: 1-373 <JAN>

A/Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AA847091.1; PID:g183943

R/Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Achwal, R.S.; Barnard, E.A.; Kunapuli, S.P.

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A/Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A/Reference number: JC4615; MUID:96158962; PMID:8579591

A/Accession: JC4615

A/Molecule type: mRNA

A/Residues: 1-373 <AYV>

A/Cross-references: GB:U42029; NID:gl147730; PIDN:AAA97872.1; PID:gl147731

A/Experimental source: erythro leukemia cells

R/Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.

submitted to the EMBL Data Library, May 1995

A/Description: Cloning of a human putative P2Y receptor.

A/Reference number: S54253

A/Accession: S54253

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-137,139-373 <LEO>

A/Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA95066.1; PID:g798836

C/Comment: This receptor belongs to a family of G protein-coupled receptors. It responds

C/Genetics:

A/Gene: P2Y1; GDB:P2RY1

A/Cross-references: GDB:677125; OMIM:601167

A/Map position: 3pter-3qter

C/Superfamily: ATP receptor P2u

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote

F/52-77/Domain: transmembrane #status predicted <TM1>

F/124-152/Domain: transmembrane #status predicted <TM3>

F/171-191/Domain: transmembrane #status predicted <TM4>

F/214-237/Domain: transmembrane #status predicted <TM5>

F/261-282/Domain: transmembrane #status predicted <TM6>

F/305-328/Domain: transmembrane #status predicted <TM7>

F/11,27,113,197/Binding site: carboxylate (Asn) (covalent) #status predicted

F/258,336/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

F/330,339/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F/343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen

Query Match 32.0%; Score 567; DB 2; Length 373;  
Best Local Similarity 36.1%; Pred. No. 6.6e-41;  
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QY 24 CTDENIPKMHYLPVYIGIIFLVGPGNAVVISYIFPMRPWKSGSTIIMLNACTDILYL 83  
DB 42 CALTKTGFQFYLPVAVYILVFIIGLGNVAIMFVFMKPSGISTYMFNLALADFLYV 101  
QY 84 TSLPFLHYVYASGENWIFGDMCKQRFIFHNLYSGILFVTCISAHRYSGVVPKSLG 143  
DB 102 LTLPALFYFNKTDWIFGDMCKLQRFIFHNLYSGILFVTCISAHRYSGVVPKSLG 161  
QY 144 IHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNTRNS-ACLDLTSSDELNTIKWNLIL 202  
DB 162 RLKKNAICISLVWLIWVAISPILFYSGTGVKKNKTIITCYDTSDEYLSRYFIYSMCT 221  
QY 203 TATTFCLPLVITLCYTTIITHTLHGLQDSCLOKARLLIILLAFYVCFPLHLRV 262  
DB 222 TVAMFCVPLVILGCGYGLIVRALYKLDNGLRKSITVILVITVFAVSYPHFVVKMT 281  
QY 263 IRIESRL---LSISCSIEHQIHEAVIVSRPLAALNTFGNLLLYVVSDFNQAVCSVTR 318  
DB 282 MNLRLARLDFQTPMCAFNDRVATYQVTRGLASLNSCVDPIYFLAGDTFRRRLSRATR 340  
RESULT 2  
S33733  
G protein-coupled receptor - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S33733  
R:Webb, T.E.; Simon, J.; Kriehak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock  
FEBs Lett. 324, 219-225, 1993  
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.  
A:Reference number: S33733; MUID:93285340; PMID:8508924  
A:Accession: S33733  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-362 <WEB>  
A:Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g3950  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor; transmembrane protein  
Query Match 31.9%; Score 565.5; DB 2; Length 362;  
Best Local Similarity 35.0%; Pred. No. 8.6e-41;  
Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;  
QY 1 MNEPLDYLANASDFDYAA---AFGN---CTDENIPKMHYLPVYIGIIFLVGPGNAV 53  
DB 1 MTEALISAALNGTQPELLAGGWAAGNATTKCSLTGTGFQFYLPVAVYILVFIIGLGN 60  
QY 54 VISTYIFKMRPWKSGSTIIMLNACTDILYLTLSPFLHYVYASGENWIFGDMCKQRFIF 113  
DB 61 ATWMEVFNHRPWSGISTYMFNLALADFLYLTLPALFYFNKTDWIFGDMCKLQRFIF 120  
QY 114 HFNLYSSILFLACSFIFRYCVIIHPMPCSFISHKTRCAVAVCAVWIIISLVAVIPMTFLI- 172  
DB 121 HVNLYSGILFLACISVHRITGVVHPVLPKSLGRKKNAVVSVALVAVIAPILFYSG 180  
QY 173 TSTNTRNSACLDLTSSDELNTIKWNLILATTTATTCPLPLVITLCYTTIITHTLHGLQTD 232  
DB 181 TGVRRNKTTICDVTDAEYLSRYFVYSMCTTVFMFCIPFIVILGCGYGLIVRALYKLDN 240  
QY 233 SCLKOKARLLIILLAFYVCFPLHLRVIRIESRL---LSISCSIEHQIHEAVIVSRP 289  
DB 241 SPERRKSYIVLIVLTVFAVSYPHFVVKMTLNLRLARLDFQTPMCAFNDKVVATYQVTRG 300  
QY 290 LAALNTFGNLLLYVVSDFNQAVCSVTR 318  
DB 301 LASLNSCVDPIYFLAGDTFRRRLSRATR 329

RESULT 3

JC4162  
P2Y receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 12-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: JC4162  
R:Henderson, D.J.; Elliott, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.  
Biochem. Biophys. Res. Commun. 212, 648-656, 1995  
A:Title: Cloning and characterization of a bovine P2Y receptor.  
A:Reference number: JC4162; MUID:95352058; PMID:7626079  
A:Accession: JC4162  
A:Molecule type: mRNA  
A:Residues: 1-373 <HEN>  
A:Cross-references: UNIPROT:P48042; EMBL:X87628; NID:gl032484; PIDN:CAA60958.1; PID:gl032  
A:Experimental source: aortic endothelial cell  
C:Genetics:  
A:Gene: bovp2y  
C:Superfamily: ATP receptor P2u  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:52-77/Domain: transmembrane #status predicted <TM1>  
F:88-111/Domain: transmembrane #status predicted <TM2>  
F:124-150/Domain: transmembrane #status predicted <TM3>  
F:171-191/Domain: transmembrane #status predicted <TM4>  
F:214-237/Domain: transmembrane #status predicted <TM5>  
F:261-282/Domain: transmembrane #status predicted <TM6>  
F:303-328/Domain: transmembrane #status predicted <TM7>  
F:11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
Query Match 31.7%; Score 562; DB 2; Length 373;  
Best Local Similarity 36.1%; Pred. No. 1.8e-40;  
Matches 108; Conservative 67; Mismatches 120; Indels 4; Gaps 2;  
QY 24 CTDENIPKMHYLPVYIGIIFLVGPGNAVVISYIFPMRPWKSGSTIIMLNACTDILYL 83  
DB 42 CALTKTGFQFYLPVAVYILVFIIGLGNVAIMFVFMKPSGISTYMFNLALADFLYV 101  
QY 84 TSLPFLHYVYASGENWIFGDMCKQRFIFHNLYSGILFVTCISAHRYSGVVPKSLG 143  
DB 102 LTLPALFYFNKTDWIFGDMCKLQRFIFHNLYSGILFVTCISAHRYSGVVPKSLG 161  
QY 144 IHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNTRNS-ACLDLTSSDELNTIKWNLIL 202  
DB 162 RLKKNAVVISLVWLIWVAISPILFYSGTGVKKNKTIITCYDTSDEYLSRYFIYSMCT 221  
QY 203 TATTFCLPLVITLCYTTIITHTLHGLQDSCLOKARLLIILLAFYVCFPLHLRV 262  
DB 222 TVAMFCVPLVILGCGYGLIVRALYKLDNGLRKSITVILVITVFAVSYPHFVVKMT 281  
QY 263 IRIESRL---LSISCSIEHQIHEAVIVSRPLAALNTFGNLLLYVVSDFNQAVCSVTR 318  
DB 282 MNLRLARLDFQTPMCAFNDRVATYQVTRGLASLNSCVDPIYFLAGDTFRRRLSRATR 340  
RESULT 4  
S68679  
G protein-coupled receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S68679  
R:Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.  
FEBS Lett. 384, 260-264, 1996  
A:Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expe  
A:Reference number: S68679; MUID:96197801; PMID:8617367  
A:Accession: S68679  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-365 <STA>  
A:Cross-references: UNIPROT:P51582; EMBL:X96597; NID:g1296631; PIDN:CAA65415.1; PID:g129  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor  
Query Match 29.0%; Score 514; DB 2; Length 365;  
Best Local Similarity 35.1%; Pred. No. 2.1e-36;

**Proc. Natl. Acad. Sci. U.S.A.** 91, 3275-3279, 1994

A>Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic  
A|Reference number: A54946; MUID:94211846; PMID:8159738

A|Accession: A54946

A>Status: preliminary

A|Molecule type: mRNA; protein

A|Residues: 1-375 <PAR>

A|Cross-references: GB:U07225

A|Note: parts of this sequence were confirmed by protein sequencing

C|Genetics:

A|Gene: GDB:P2RY2; HP2U; p2U

A|Cross-references: GDB:362713; OMIM:600041

A|Map position: liq13.5-ilql4.1

C|Superfamily: ATP receptor P2u

C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match                24.7%; Score 438; DB 2; Length 375;  
Best Local Similarity     33.0%; Pred. NO. 6.7e-30;  
Matches      93; Conservative    59; Mismatches 118; Indels    12; Gaps    4;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 28  | NIPKMHVLPVIYGIIFLGFPGNAVISTITFKMPKWKSITIEMNLACTDLYLTSLP   | 87  |
| Dd | 28  | NEDFKVLPLVSYGVCVGLCLNAGLIYFLCRKTWASTTMMFHLAVSDALYLASLP    | 87  |
| Qy | 88  | FIIHYAGENWIIGDFGCKFIIRSFHFNLSILFLTCSIFRYCVIHPMCSFSIKHT    | 147 |
| Dd | 88  | LIVTYARGDHWPFTLVLCKLVRFLFYTNLYCSILFLTCTSVHRCLGVLRPLRSRWGA | 147 |
| Qy | 148 | RCVVACAAVMIIISIAVAVIPMTFLTSTNRHSACLDTSSDELNTWKYNLLITATTF  | 207 |
| Dd | 148 | RVARVAGAVALVLAQAAPVLIFYVTTSAR-GELTCDDTSAPELFRFAYSVMGLLF   | 206 |
| Qy | 208 | CLPIVTVTLCTTIITHLT-----THGITQDSCLKOKARRLTILLILAFCVCPFPFIL | 260 |
| Dd | 207 | AVPEAVILVCVLMARRLLKPAYGISGGLP---AKGSVRTIAVLAVAFCLPFPHVT   | 263 |
| Qy | 261 | RVIESRLSISCIENIQIEHAITYVSRPLAINTFGNLLY                    | 302 |
| Dd | 264 | RTLYESRSLDSLCHTLNAINMAKVTR-LAGANSCLDPVLY                  | 304 |

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RESULT 7
I55450
G protein-coupled P2 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55450
R:Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A:Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.
A:Reference number: I55450; MUID:96064682; PMID:7592819
A:Accession: I55450
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <RES>
A:Cross-references: UNIPROT:Q63317; GB:D63665; NID:gi066007; PID:gi06600
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor

Query Match      23.9%; Score 423; DB 2; Length 328;
Best Local Similarity 32.9%; Pred. No. 1.1e-28;
Matches 96; Conservative 44; Mismatches 126; Indels 26; Gaps 5;

QY 36 LPVIYGIIFVGGPNNAWLTSTYIFKMPKWSSTIIMLNACTDLYLTSLPLIHYAS 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 29 LPPVYSVLVGLPLNVCVIAQICASRRTLTRSAVYTLNALADLLYACSLPLIYNAR 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 96 GENWIFGDFMCKTIRFSFHNLYSILFTCSIPRYCVIIHPMCSFSIHK---TRCAVV 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 GDHWPPGDLACRLVRFLFYANLHGSILFTCISIPQYILGICHPAPW--HKRGGRAAWV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 ACAVWIIISLVAVIPMTFLTSTNRTNRSACLDITSSDELNTIKWYNLILTATTCPLV 212
   | : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 147 VCGVWLVNTAQCPLTAVFAATGICQNRRTVCYDLSPPLSTLYLPCYGMALTVIGFLPFT 206  
QY 213 IVTLCTTTIHTLTHGLQDSC-----LQKARLTLILLAFYVCFPLPHIL 260  
Db 207 ALLACYCRMARLL-----CRQDGPAGPVAQERRSKAARMVAAVVFISFLPPHIT 258  
QY 261 RVIRIESRL--SISCSIEHQIHEAYIVSRPLAALNTFGNLLLVVVSDFNQ 311  
Db 259 KTAIVLRSTPGVSCPVLTFFAAYKGTFRPASNSVLDILFFYTOQKFR 310  
RESULT 8  
151667  
Thrombin receptor - African clawed frog  
C;Species: *Xenopus laevis* (African clawed frog)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: J51667  
R;Gerszten, R.E.; Chen, J.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; C  
Nature 368, 648-651, 1994  
A;Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac  
A;Reference number: 151667; MUID:94195429; PMID:8145852  
A;Accession: J51667  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-420 <GER>  
A;Cross-references: UNIPROT:P47749; EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g4951

Query Match 23.7%; Score 419.5; DB 2; Length 420;  
Best Local Similarity 31.1%; Pred. No. 2.9e-28;  
Matches 93; Conservative 73; Mismatches 108; Indels 25; Gaps 7;  
QY 35 YLPVYIGIIFLVGPGNAVISTYIFKMRPKSSTIIMLNACTDLYLTLSPFLIHYA 94  
Db 103 FVPSLYTVFVIGLPLNLALIIIFKMKRKPAAVYMLNLAIDVFSVLPKIAHL 162  
QY 95 SGENWIFGDFMCKTFRFSHFENLYSSILFCTFSIFRYCVIIHPMCSFCSIHKTRCAVVC 154  
Db 163 SGNDLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRELAIVYPMHLSLWRTMSRAYMAC 222  
QY 155 AVVWIIISLVAVIPMTFLTSTNRTNRSACLDLTSSDELNTIK-----WYNLLLTATTCFL- 209  
Db 223 SFIWLISASTIPLV-----TEQTKIPRLDITTCCHVDLDLKDQFY--IYFSSFCLL 276  
QY 210 ----PLVTITLCYTTIHTLTHGLQDSCQKARRLTILLAFYVCFPLPHILRVIRI 265  
Db 277 FFFVPIITTCYIGIISLSSSIENCKKTRALFLAVVLCVFIICFGPTNL-----331  
QY 266 ESRLISCSIEHQIHEAYIVSRPLAALNTFGNLLLVVVSDFNQAVCVSTVRC-KVS 322  
Db 332 --FLTHVQBANEFLYAYILSACVGSVSCCLDPLIYVYASSQCCQRYLYSLCCRKVS 387  
RESULT 9  
JC4800  
P2Y6 receptor - human  
C;Species: *Homo sapiens* (man)  
C;Date: 15-Oct-1995 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: JC4800; G02514  
R;Communi, D.; Parmentier, M.; Boeynaems, J.M.  
Biochem. Biophys. Res. Commun. 222, 303-308, 1996  
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept  
A;Reference number: JC4800; MUID:96222498; PMID:8670200  
A;Accession: JC4800  
A;Molecule type: mRNA  
A;Residues: 1-328 <COM>  
A;Cross-references: UNIPROT:Q15077; EMBL:X97058  
A;Experimental source: placenta  
R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: H01373  
A;Accession: G02514  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA

A;Residues: 'M',4-328 <HAM>  
A;Cross-references: EMBL:U52464; NID:gl407632; PIDN:AAB03572.1; PID:gl407633  
C;Genetics:  
A;Gene: P2Y6  
C;Superfamily: ATP receptor P2u  
C;Keywords: glycoprotein; placenta; receptor; transmembrane protein  
F;26-52/Domain: transmembrane #status predicted <TMM1>  
F;63-86/Domain: transmembrane #status predicted <TMM2>  
F;104-122/Domain: transmembrane #status predicted <TMM3>  
F;143-167/Domain: transmembrane #status predicted <TMM4>  
F;193-216/Domain: transmembrane #status predicted <TMM5>  
F;241-264/Domain: transmembrane #status predicted <TMM6>  
F;283-305/Domain: transmembrane #status predicted <TMM7>  
F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.9%; Score 405; DB 2; Length 328;  
Best Local Similarity 32.6%; Pred. No. 3.8e-27;  
Matches 94; Conservative 44; Mismatches 140; Indels 10; Gaps 4;  
QY 32 KMHLPVYIGIIFLVGPGNAVISTYIFKMRPKSSTIIMLNACTDLYLTLSPFLI 91  
Db 25 KQLLPVYSVLAAGLPLNICVITQICTSRRALTRTAVYTLNLALDLYACSLPLIIY 84  
QY 92 YYASGENWIFGDFMCKTFRFSHFENLYSSILFCTFSIFRYCVIIHPMCSFCSIHK---TR 148  
Db 85 NYAQGDHWPFGDFACRLVRFELFYANLHGSILFCTISFQRYLGLCHPLAPW--HRRGRR 142  
QY 149 CAVVACAVVWIIISLVAVIPMTFLTSTNRTNRSACLDLTSSDELNTIKWNLILTATTC 208  
Db 143 AMLVLCVAVWMLVNTQCLPTAIPAATGICQNRRTVCYDLSPALATHYMPYGMALTVIGFL 202  
QY 209 LPLVITLCYTTIHTLTHGLQDSCQK---KARLTILLAFYVCFPLPHILRVIR 264  
Db 203 LPPAALLACYLLACRLCRQDGPAPVPAQERRKAARMVAAVFAISFLPHITKTAY 262  
QY 265 IESRL--SISCSIEHQIHEAYIVSRPLAALNTFGNLLLVVVSDFNQ 311  
Db 263 LAVRSTFGVPCVLEAFAAAYKGTFRFPASNSVLDPLIFTQKFR 310  
RESULT 10  
SI7148  
alpha-thrombin receptor - Chinese hamster  
C;Species: *Cricetus griseus* (Chinese hamster)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: SI7148  
R;Rasmussen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani  
FEBS Lett. 288, 123-128, 1991  
A;Title: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca(2  
A;Reference number: SI7148; MUID:91348247; PMID:1652467  
A;Accession: SI7148  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-427 <RAS>  
A;Cross-references: UNIPROT:Q00991; EMBL:X61958; NID:g940495; PIDN:CAA43957.1; PID:g4953  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.4%; Score 397; DB 2; Length 427;  
Best Local Similarity 28.4%; Pred. No. 2.4e-26;  
Matches 95; Conservative 75; Mismatches 141; Indels 24; Gaps 6;  
QY 10 NASDPDYAAAFNGCTDNIPLKMH-----YLPVYIGIIFLVGPGNAV 53  
Db 65 NESTLPEGRAIYLNKSHSPAPLAPFISEDAGSYLTPWLRFLIPSVYTFVVFVSPLNLL 124  
QY 54 VISTYIFKMRPKSSTIIMLNACTDLYLTLSPFLIHYASGENWIFGDFMCKTFRFSF 113  
Db 125 ATAVFVLKMKKPAVAVYMLHLMADVLVSVLPKISYFSGSDMQFSGMCRATAAF 184  
QY 114 HENLYSSILFCTFSIFRYCVIIHPMCSFCSIHKTRCAVVCVAVVWIIISLVAVIPMTFLT 173  
Db 185 YCNMYASIMLTVISIDRFLAVVYFIQSLSWRTIGRANFTCLVWMAIMGVVPL--LLKE 243



QY 174 STNRT---NRSACLDLTSSDELNTI-KWYNLILTATTFCPLPVIVVLCYTTIHTLTHGL 229  
Db 244 QTRVPEGLNITTCVDLNLTEGQFYYSFSAVFLVPLIISICYMSIIRCLSSSS 303  
QY 230 QTDSCCLKQKARLTLTLLAFVVCFLPFHLIRVIRIESRLSISCSIEHQIHEAVIVSRP 289  
Db 304 VANRKSGRALFLSAVFCVFCVGTNVLITMHY--LLSDSPATE-KAYFAYLLVCV 360  
QY 290 LAALNTFGLNLLYVVDNFFQAVCVSTVRCKVSGN 324  
Db 361 VTSVSCIDPLIYYASSECQTLGILCKESSD 395  
RESULT 11  
A43448  
thrombin receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A43448  
R:Zhong, C.; Hayzer, D.J.; Corson, M.A.; Runge, M.S.  
J. Biol. Chem. 267, 16975-16979, 1992  
A:Title: Molecular cloning of the rat vascular smooth muscle thrombin receptor. Evidence  
A:Reference number: A43448; MUID:92381002; PMID:1324917  
A:Accession: A43448  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-432 <ZHO>  
A:CROSS-references: UNIPROT:P26824; GB:M81642; NID:G207465; PIDN:AAA2274.1; PID:G207466  
A:Experimental source: RASM aortic smooth muscle cells  
A>Note: sequence extracted from NCBI backbone (NCBI:111973, NCBI:111974)  
C:Keywords: G protein-coupled receptor; transmembrane protein  
Query Match 22.4%; Score 396.5; DB 2; Length 432;  
Best Local Similarity 29.6%; Pred. No. 2.7e-26;  
Matches 99; Conservative 74; Mismatches 141; Indels 21; Gaps 8;  
QY 4 PLD-----VLANSDPPDYAA-----AFNGCTDENIPKMHYLPVIGIIFLVGPPGNA 52  
Db 73 FLEGRVFL-NKSRPPPPPPPFISDASGYLTPWLTL---FIPSVYTFVIVSLPLNI 128  
QY 53 VVISTYIFKMRPKWKSSTIIMNLACTDLYLTLSPFLHYHAGENWIFGDMCKFIKPS 112  
Db 129 LAIAVVFVRMKVPAVVMHGLMADVLVSLPFLKISYYPGSDWQFGSGMCRFATAA 188  
QY 113 FPHNLYSSILFTCSIFRYCVIIHPMCSFISIKRCAVAVCAVVMIIISLVAVIMTF-- 170  
Db 189 CVCNMYASIMLMTVLSIDFLAVVPIQSLSWRTIGRANFTCVIWMVAVGVPELLKE 248  
QY 171 LITSTNRNRSACLDLTSSDELNTI-KWYNLILTATTFCPLPVIVVLCYTTIHTLTHGL 229  
Db 249 QTTQVPEGLNITTCVDLNLTEGQFYYSFSAVFLVPLIISICYMSIIRCLSSSA 308  
QY 230 QTDSCCLKQKARLTLTLLAFVVCFLPFHLIRVIRIESRLSISCSIEHQIHEAVIVSRP 289  
Db 309 VANRKSGRALFLSAVFCVFCVGTNVLITMHY--LLSDSPGTE-TAYFAYLLVCV 365  
QY 290 LAALNTFGLNLLYVVDNFFQAVCVSTVRCKVSGN 324  
Db 366 VTSVSCIDPLIYYASSECQKHLISILCKESSD 400  
RESULT 12  
148705  
proteinase activated receptor 2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 148705  
R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.  
J. Biol. Chem. 270, 5950-5955, 1995  
A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and  
A:Reference number: 148705; MUID:95197620; PMID:7890726  
A:Accession: 148705  
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-399 <RES>  
A:CROSS-references: UNIPROT:P55086; EMBL:Z48043; NID:G663020; PIDN:CAA88097.1; PID:G66303  
C:Superfamily: ATP receptor P2u  
Query Match 21.9%; Score 388.5; DB 2; Length 399;  
Best Local Similarity 29.9%; Pred. No. 1.2e-25;  
Matches 97; Conservative 65; Mismatches 129; Indels 33; Gaps 9;  
QY 35 YLPVIYGIIFLVGPPGNAVISTYIFKMRPKWKSSTIIMNLACTDLYLTLSPFLHYHVA 94  
Db 79 FLPVVYIIIVFVIGLPSNGMALWIFLRTKKKHPAVIYMANLALADLLSWPEPKISYHL 138  
QY 95 SGENWIFGDMCKFIKPSFHNLYSILFTCSIFRYCVIIHPMCSFISIKRCAVAVAC 154  
Db 139 HGNWVYGEALCKVLIGFFYGNMYSILFTCLSVQRYVWVIVNPMG---HPRKKANIAV 194  
QY 155 AV---VWIIISLVAVIM-----TFLITSTNRNRSACLDLTSSDEL-NTIKWNILITAT 205  
Db 195 GVSALAILLPLVITPLVYMKQTIYIPALNIT---TCHDVLPEEVLVGDMFNYSLSAIG 251  
QY 206 TFCPLPVIIVLCYTTIIMTLTHGLQTDCLK--QKARLTLTLLAFVYVCFPLFLHRLVI 263  
Db 252 VFLFPALLTASAYVLMIKTLRSSAMDEHSEKKRQRAIRLIITVLAIFYFCFAPSLLVW 311  
QY 264 RIESRLLSISCSIEHQIHEAVIVSRPLAALNTFGLNLLYVVDNFFQ-----AVCSTVR 318  
Db 312 ---HYFLIKTORQSHVVALYVALCLSTLNSCIDPFVYVFSVKDFRDHARNALLCSVR 367  
QY 319 -----CKVSGNLEQAKKISYSNN 336  
Db 368 TVNRMQISLSSNKPFSKSGSYSS 391  
RESULT 13  
A37912  
thrombin receptor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: A37912  
R:Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.  
Cell 64, 1057-1068, 1991  
A:Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic  
A:Reference number: A37912; MUID:91168254; PMID:1672265  
A:Accession: A37912  
A:Molecule type: mRNA  
A:Residues: 1-425 <VUA>  
A:CROSS-references: UNIPROT:P25116; GB:M62424; NID:G339676; PIDN:AAA36743.1; PID:G339677  
C:Genetics:  
A:Gene: GDB:F2R  
A:CROSS-references: GDB:127737; OMIM:187930  
A:Map position: 5q13-5q13  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-425/Product: thrombin receptor #status predicted <MAT>  
Query Match 21.9%; Score 388.5; DB 2; Length 425;  
Best Local Similarity 29.3%; Pred. No. 1.3e-25;  
Matches 93; Conservative 70; Mismatches 133; Indels 21; Gaps 6;  
QY 35 YLPVIYGIIFLVGPPGNAVISTYIFKMRPKWKSSTIIMNLACTDLYLTLSPFLHYHVA 94  
Db 104 FVPSYITGVFVSLPLNIALVWFLKMKVKKPAVVMHGLATADVLSVLPFKISYIF 163  
QY 95 SGENWIFGDMCKFIKPSFHNLYSILFTCSIFRYCVIIHPMCSFISIKRCAVAVAC 154  
Db 164 SGSDWQFSGELCRFVTAFAFYCNMVASILLMTVISIDRLAVVYPMQSLSWTLGRASFTC 223  
QY 155 AVWIIISLVAVIM-----TFLITSTNRNRSACLDLTSSDEL-NTIKWNILITATTC 208  
Db 224 LAIWALAIAGVVPVLVKEQITQVPLNIT---TCHDVLNETLLEGYVAYVPSAFSAVFFF 280  
QY 209 LPLVIVLCYTTIIMTLTHGLQTDCLKQKARLTLTLLAFVYVCFPLFLHRLVIRIESR 268

Db 281 VPLIISTVCVSIIRCLSSAVANRSKSRALFSLAAVFCIFICFGPTNVLIAHY-- 338  
QY 269 LLSISCSIEHQHEAYIVSRPLAALNTFGNLLYVVVSDNFQQAQVCTVCK----- 320  
Db 339 FLGTSSTTE-AAVFAVLLVCVSSISSCIDPLIYVYASSECQVYVYSLCKESSDPSSY 397  
QY 321 -VSGNLEQAKKISYSNN 336  
Db 398 NSSGQLMASKMDTCSSN 414  
RESULT 14  
I50241  
G protein-coupled receptor 6H1 - chicken  
N;Alternate names: purinoceptor 6H1  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50241; J04618  
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
J. Immunol. 151, 628-636, 1993  
A;Title: Identification of a G protein coupled receptor induced in activated T cells.  
A;Reference number: I50241; MUID:93329058; PMID:8393036  
A;Accession: I50241  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-308 <KAP>  
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.  
Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
A;Reference number: J04618; MUID:96190677; PMID:8619790  
A;Accession: J04618  
A;Molecule type: mRNA  
A;Residues: 1-308 <WEB>  
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
A;Experimental source: T-cells  
C;Comment: This receptor plays a role in T-cell activation.  
C;Genetics:  
A;Gene: p2Y5  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein  
F;15-40/Domain: transmembrane #status predicted <TM2>  
F;51-74/Domain: transmembrane #status predicted <TM2>  
F;89-109/Domain: transmembrane #status predicted <TM3>  
F;133-183/Domain: transmembrane #status predicted <TM4>  
F;177-201/Domain: transmembrane #status predicted <TM5>  
F;227-248/Domain: transmembrane #status predicted <TM6>  
F;269-292/Domain: transmembrane #status predicted <TM7>  
Query Match 21.5%; Score 380; DB 2; Length 308;  
Best Local Similarity 30.8%; Pred. No. 4.9e-25;  
Matches 90; Conservative 58; Mismatches 134; Indels 10; Gaps 6;  
QY 23 NCTDENIPKMHYLVYIGIIFLVGPGNAVVIYIFKMRPKWSSTIIMNLACTDLY 82  
Db 5 NCSTED-SFKYTLGCVFSWVFVGLIANCAVYIFTLKVNETTTVMNLALSLLF 63  
QY 83 LTSPLFLHYASGENWIFGDMCKFIKFSFHNLYSSILFLTCFSIPRYCVIIHPMSCF 142  
Db 64 VFTLFRYFYFV-RNWPFGDVLKISVTLFTNNYGSILFLTCISVDRFLAIVHFRSK 122  
QY 143 SHKTRCAVACAVVWIIISLVAIVPMTFLTITSTNRSACLDTSSDELNTIKWY--- 198  
Db 123 TLTKRNARIVCAVWITVLAGSTPASP-FQSTNQNTQEQTCFENPESTWKYLSRI 181  
QY 199 NILITATTCLPLIVITLCYTTIHTLTH--GLQDSCCLKQKARLITILLAFVVCFLP 256  
Db 182 VIFIEIVGFPIILINVTCTWVLRNLKPLSLRNLKSKKVKLMIFVHLVIFCFVFP 241  
QY 257 FHLRVIRIESRLLS-ISCSEIQHEAYIVSRPLAALNTFGNLLYVVVSD 307  
Db 242 YNITILYSLMRQTWTWNCVSVVAVRTWVPTLCIAVSNCCFPDIVVYFTSD 293

RESULT 15  
B45680  
G protein-coupled peptide receptor EBI 2 - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B45680  
R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.  
J. Virol. 67, 2209-2220, 1993  
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p  
A;Reference number: A45680; MUID:93188173; PMID:8383238  
A;Accession: B45680  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-361 <BIR>  
A;Cross-references: UNIPROT:P32249; GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057  
A;Experimental source: B-lymphocytes  
A;Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBI:P:127097)  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein  
Query Match 21.3%; Score 376.5; DB 2; Length 361;  
Best Local Similarity 26.9%; Pred. No. 1.1e-24;  
Matches 92; Conservative 70; Mismatches 159; Indels 21; Gaps 7;  
QY 11 ASDP-PDYAAAFNGCTDENIPLKMHY-----LPVIYIGIIFLVGPGNAVVIYIFKMR 63  
Db 6 ANNTPSATPQGNDCD---LYAHSTARIWMLPHYSLVFIIGLVGNLLALVVIVQNRK 61  
QY 64 PKWSSTIIMNLACTDLYLTSPLFLHYASGENWIFGDMCKFIKFSFHNLYSSILF 123  
Db 62 KINSTLYSTNLVISDILFTALPTRIAYVAMGDFWRIGDALCRITALVIFYINTYAGVNF 121  
QY 124 LTCFSIPRYCVIIHPMSCFSIHKTRCAVACAVVWIIISLVAIVPMTFLTITSTNRSAC 183  
Db 122 MTCLSIDRFTAVVHPLRYNKKRIEHAQGVIFWILVFAQTLLPINPMKQAEARITC 181  
QY 184 LDLTSSDELNTIKWYNILITATTCLPLIVITLCYTTIHTL-----THGLQDSCCLKQK 238  
Db 182 MEYFNFEETKSLPMLLIGACFIVGVLPILIIICVQICCKLFRKAKQNPLTEKSGVNRK 241  
QY 239 ARRLTILLALAFYVCFPLPFLHVRIRIESRLLSISCSEIE-NQIHEAYIVSRPLAALNTFG 297  
Db 242 ALNTIILIIIVVFLCFTPYHV-AIQHMKKLRFSNLFECQSRHSFQISLHFTVTCIMNPN 300  
QY 298 ---NLLLVVVSDNFQQAQVCTVCKVSGNLEQAKKISYSNN 336  
Db 301 CCMDFPIYFFACKGYKRWMLKQVSVSISAVKSAPEEN 342  
Search completed: October 29, 2004, 15:05:21  
Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2004, 14:16:02 ; Search time 192 Seconds  
(without alignments)  
1009.902 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVGNLEQAKKISVNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID           | Description         |
|------------|-------|---------------|--------|--------------|---------------------|
| 1          | 1771  | 100.0         | 337    | 1 GP80_HUMAN | Q96p68 homo sapien  |
| 2          | 1495  | 84.4          | 337    | 2 Q61YF8     | Q61yf8 mus musculu  |
| 3          | 1495  | 84.4          | 337    | 2 AAT10591   | Aat10591 mus muscu  |
| 4          | 1487  | 84.0          | 337    | 2 Q6Y1R5     | Q6y1r5 rattus norv  |
| 5          | 1487  | 84.0          | 337    | 2 AAP32736   | Aap32736 rattus no  |
| 6          | 579   | 32.7          | 373    | 2 Q8BMJ5     | Q8bmj5 mus musculu  |
| 7          | 577.5 | 32.6          | 357    | 2 Q9DE05     | Q9de05 raja erinac  |
| 8          | 576   | 32.5          | 373    | 1 P2YR_CAVPO | P49650 mus musculu  |
| 9          | 575   | 32.5          | 373    | 1 P2YR_MOUSE | Bac28413 mus muscu  |
| 10         | 575   | 32.5          | 373    | 2 BAC28413   | Bac28413 mus muscu  |
| 11         | 575   | 32.5          | 373    | 2 BAC29506   | Bac29506 mus sapien |
| 12         | 567   | 32.0          | 373    | 1 P2YR_HUMAN | P47900 homo sapien  |
| 13         | 565.5 | 31.9          | 362    | 1 P2YR_CHICK | P34996 gallus gall  |
| 14         | 565.5 | 31.9          | 362    | 1 P2YR_MELGA | P49652 meleagris g  |
| 15         | 565   | 31.9          | 373    | 1 P2YR_RAT   | P49651 rattus norv  |
| 16         | 562   | 31.7          | 373    | 1 P2YR_BOVIN | P48042 bos taurus   |
| 17         | 559   | 31.6          | 537    | 2 Q7ZW07     | Q7zwq7 xenopus lae  |
| 18         | 557   | 31.5          | 537    | 1 P2Y8_XENLA | P79928 xenopus lae  |
| 19         | 556.5 | 31.4          | 361    | 2 Q90X57     | Q90x57 xenopus lae  |
| 20         | 547   | 30.9          | 347    | 2 O57466     | O57466 meleagris g  |
| 21         | 537   | 30.3          | 374    | 2 Q7ZZA4     | Q7zza4 brachydanio  |
| 22         | 532.5 | 30.1          | 349    | 2 Q6P852     | Q6p852 xenopus tro  |
| 23         | 532.5 | 30.1          | 349    | 2 AAH61378   | AAh61378 xenopus t  |
| 24         | 514   | 29.0          | 365    | 1 P2Y4_HUMAN | P51582 homo sapien  |
| 25         | 512   | 28.9          | 361    | 1 P2Y4_RAT   | O35811 rattus norv  |
| 26         | 503   | 28.4          | 361    | 1 P2Y4_MOUSE | O31j57 mus musculu  |
| 27         | 503   | 28.4          | 361    | 2 BAC36314   | Bac36314 mus muscu  |
| 28         | 492   | 27.8          | 328    | 1 P2Y3_CHICK | Q89907 gallus gall  |
| 29         | 488.5 | 27.6          | 317    | 2 Q61YF9     | Q61yf9 rattus norv  |
| 30         | 488.5 | 27.6          | 317    | 2 AAT10590   | Aat10590 rattus no  |
| 31         | 487.5 | 27.5          | 346    | 1 CLT2_HUMAN | Q9ns75 homo sapien  |

|    |       |      |     |              |                    |
|----|-------|------|-----|--------------|--------------------|
| 32 | 487.5 | 27.5 | 346 | 2 AAH69160   | AAh69160 homo sapi |
| 33 | 486.5 | 27.5 | 328 | 1 P2Y3_MELGA | O93361 meleagris g |
| 34 | 483.5 | 27.3 | 374 | 1 P2Y2_RAT   | P41232 rattus norv |
| 35 | 483.5 | 27.3 | 374 | 2 AAH61754   | AAh61754 rattus no |
| 36 | 479   | 27.0 | 330 | 1 GP91_HUMAN | Q9bxa5 homo sapien |
| 37 | 479   | 27.0 | 373 | 1 P2Y2_MOUSE | P35383 mus musculu |
| 38 | 474   | 26.8 | 377 | 1 P2Y2_HUMAN | P41231 homo sapien |
| 39 | 452   | 25.5 | 345 | 1 CLT2_PIG   | Q95n03 sus scrofa  |
| 40 | 445.5 | 25.2 | 309 | 2 Q8RS28     | Q8r528 mus musculu |
| 41 | 442.5 | 25.0 | 309 | 1 CLT2_MOUSE | Q920a1 mus musculu |
| 42 | 430   | 24.3 | 309 | 1 CLT2_RAT   | Q924t9 rattus norv |
| 43 | 423   | 23.9 | 328 | 1 P2Y6_RAT   | Q63371 rattus norv |
| 44 | 423   | 23.9 | 328 | 2 AAH72520   | AAh72520 rattus no |
| 45 | 421   | 23.8 | 328 | 1 P2Y6_MOUSE | Q9erk9 mus musculu |

## ALIGNMENTS

### RESULT 1

GP80\_HUMAN STANDARD; PRT; 337 AA.  
AC Q96P68; Q86TL1;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Probable G protein-coupled receptor GPR80 (P2Y-like nucleotide  
DE receptor) (P2Y-like GPCR).  
GN Name=GPR80; Synonyms=GPR99;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;  
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhiko O.,  
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;  
RT "Discovery and mapping of ten novel G protein-coupled receptor  
RT genes";  
RL Gene 275:83-91 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX PubMed=12098360;  
RA Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.-J.,  
RA Schaller H.C., Hampe W.;  
RT "GPR99, a new G protein-coupled receptor belonging to a new subgroup  
RT of nucleotide receptors";  
RL BMC Genomics 3:17-17(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22040266; PubMed=12044878;  
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;  
RT "Identification of G protein-coupled receptor genes from the human  
RT genome sequence";  
RL FEBS Lett. 520:97-101(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,  
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;  
RT "Genome-wide discovery and analysis of human seven transmembrane helix  
RT receptor genes";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thyroid;  
RA Brues M., Bonisch H., von Kugelgen I.;  
RT "Molecular cloning and functional characterization of a new human P2Y  
RT receptor";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Detected in kidney and, to a lower extend, in  
CC placenta. Not detected in brain tissues including the frontal  
CC cortex, caudate putamen, thalamus, hypothalamus, hippocampus or  
CC pons.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; AF411109; AAL26480.1; -  
DR EMBL; AF370886; AAM76912.1; -  
DR EMBL; AB083598; BAB89311.1; -  
DR EMBL; AB065877; BAC06095.1; -  
DR EMBL; AJ305372; BAC83857.1; -  
DR Genew; HGNC:4531; GPR80.  
DR MIM; 606922; -  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR002286; P2\_purnocptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; FALSE\_NEG.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
FT DOMAIN 1 34 Extracellular (Potential).  
FT TRANSMEM 35 55 1 (Potential).  
FT DOMAIN 56 69 Cytoplasmic (Potential).  
FT TRANSMEM 70 90 2 (Potential).  
FT DOMAIN 91 116 Extracellular (Potential).  
FT TRANSMEM 117 137 3 (Potential).  
FT DOMAIN 138 151 Cytoplasmic (Potential).  
FT TRANSMEM 152 172 4 (Potential).  
FT DOMAIN 173 201 Extracellular (Potential).  
FT TRANSMEM 202 222 5 (Potential).  
FT DOMAIN 223 242 Cytoplasmic (Potential).  
FT TRANSMEM 243 263 6 (Potential).  
FT DOMAIN 264 284 Extracellular (Potential).  
FT TRANSMEM 285 305 7 (Potential).  
FT DOMAIN 306 337 Cytoplasmic (Potential).  
FT DISULFD 106 183 By similarity.  
FT CARBOHYD 10 10 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 23 23 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 176 176 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 179 179 N-linked (GlcNAc. .) (Potential).  
FT CONFLICT 14 14 F -> L (in Ref. 5).  
FT CONFLICT 236 236 K -> R (in Ref. 5).  
SQ SEQUENCE 337 AA; 38251 MW; 6814EA0044756CE6 CRC64;

Query Match 100.0%; Score 1771; DB 1; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.3e-112;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNNAVISTYIF 60  
DB 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNNAVISTYIF 60  
QY 61 KMRPKWSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSFHNLYSS 120  
DB 61 KMRPKWSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSFHNLYSS 120  
QY 121 ILFLFCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180  
DB 121 ILFLFCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180  
QY 181 SACLDTSSDELNTIKWYNILITATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACLDTSSDELNTIKWYNILITATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFYVCFLPFHLRVRIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFYVCFLPFHLRVRIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSNDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSNDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337

RESULT 3  
AAT10591  
ID AAT10591 PRELIMINARY; PRT; 337 AA.  
AC AAT10591;

DB 241 RLTIILLAFYVCFLPFHLRVRIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSNDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSNDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337

# RESULT 2

QY Q61YF8 PRELIMINARY; PRT; 337 AA.  
AC Q61YF8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE G-protein-coupled receptor 99.  
GN Name=Gpr39;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA He W., Miao F.J.P., Lin D.C.H., Schwandner R.T., Wang Z., Gao J.,  
RA Chen J.-L., Tian H., Ling L.;  
RT "Citric Acid Cycle Intermediates as Ligands for Orphan G-Protein-  
RT Coupled Receptors.";  
RL Nature 0.0-0(2004)  
DR EMBL; AY612852; AAT10591.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR002286; P2\_purnocptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PRINTS; PR01157; P2\_PURNOCPTOR.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 337 AA; 38230 MW; 079A603551112277 CRC64;

Query Match 84.4%; Score 1495; DB 2; Length 337;  
Best Local Similarity 85.5%; Pred. No. 1.6e-93;  
Matches 288; Conservative 13; Mismatches 36; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNNAVISTYIF 60  
DB 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNNAVISTYIF 60  
QY 61 KMRPKWSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSFHNLYSS 120  
DB 61 KMRPKWSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSFHNLYSS 120  
QY 121 ILFLFCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180  
DB 121 ILFLFCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180  
QY 181 SACLDTSSDELNTIKWYNILITATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACLDTSSDELNTIKWYNILITATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFYVCFLPFHLRVRIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFYVCFLPFHLRVRIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSNDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSNDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337

```
DT 20-MAY-2004 (TrEMBLrel. 27, Created)
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE G-protein-coupled receptor 99.
GN GPR99.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA He W., Miao F.J.P., Lin D.C.H., Schwandner R.T., Wang Z., Gao J.,
RT "Citric Acid Cycle Intermediates as Ligands for Orphan G-Protein-
RT Coupled Receptors";
RL Nature 0:0-0(2004).
DR EMBL; AY612852; AAT10591.1; -.
SQ SEQUENCE 337 AA; 38230 MW; 079A603551112277 CRC64;

Query Match 84.4%; Score 1495; DB 2; Length 337;
Best Local Similarity 85.5%; Pred. No. 1.6e-93;
Matches 288; Conservative 13; Mismatches 36; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGFGNNAVISTYIF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MIEPLDSPASDSDFLDYPSALNGCTDEQISFKQYLPVIYGIIFLVGFGNNAVISTYIF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 KMRPWKSSIIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFRFSPHFNYLSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 KMRPWKSGTIVIMNLALTDLTYLTSPLFIHYASGENWIFGDMCKFRFSPHFNYLSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 ILFLTCSLFRVIVIIHPMSCFSIQKTRWAVVACAGWVISLVAVMPMTFLTSTNRTNR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 SACLDLTSSDELTIKWYNLIITATTCFLPLVIVTLCYTTIITLTHGLQDSCLOKAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 SACLDLTSSDDLTIKWYNLIITATTCFLPLVIVTLCYTTIITLTHGPRTHSCFKOKAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 RLTIILLAFYVCFPLPFHILVRIRIESRLLSISCSIESIENIHEAYIVSRPLAALNTFGNLL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 RLTIILLAFYVCFPLPFHILVRIRIESRLLSISCSIESIENIHEAYIVSRPLAALNTFGNLL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 LVVVSDNFQQAQVCSVTRCKVSGNLEQAQKISVSNPP 337
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 LVVVSNPFQQAQVCSVTRCKVSGNLEQAQKISVSNPP 337
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q6Y1R5 PRELIMINARY; PRT; 337 AA.
AC Q6Y1R5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE G protein-coupled receptor 80.
GN Name=Gpr80;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15001573;
RA Inbe H., Watanabe S., Miyawaki M., Tanabe E., Encinas J.A.;
RT "Identification and Characterization of a Cell-Surface Receptor,
RT P2Y15, for AMP and Adenosine";
RL J. Biol. Chem. 279:19790-19799(2004).
DR EMBL; AY191367; AAP32736.1; -.
SQ SEQUENCE 337 AA; 38377 MW; 9899E80DE0531CB9 CRC64;

Query Match 84.0%; Score 1487; DB 2; Length 337;
Best Local Similarity 85.8%; Pred. No. 5.5e-93;
Matches 289; Conservative 10; Mismatches 38; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGFGNNAVISTYIF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MIEPLDSPASDSDFLDYITALENCTDEQISFKQYLPVIYGIIFLVGFGNNAVISTYIF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 KMRPWKSSIIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFRFSPHFNYLSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 KMRPWKSSIIIMNLALTDLTYLTSPLFIHYASGENWIFGDMCKFRFSPHFNYLSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 ILFLTCSLFRVIVIIHPMSCFSIQKTRWAVVACAGWVISLVAVMPMTFLTSTNRTNR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 SACLDLTSSDELTIKWYNLIITATTCFLPLVIVTLCYTTIITLTHGLQDSCLOKAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 SACLDLTSSDDLTIKWYNLIITATTCFLPLVIVTLCYTTIITLTHGPRTHSCFKOKAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 RLTIILLAFYVCFPLPFHILVRIRIESRLLSISCSIESIENIHEAYIVSRPLAALNTFGNLL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 RLTIILLAFYVCFPLPFHILVRIRIESRLLSISCSIESIENIHEAYIVSRPLAALNTFGNLL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 LVVVSDNFQQAQVCSVTRCKVSGNLEQAQKISVSNPP 337
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 LVVVSNPFQQAQVCSVTRCKVSGNLEQAQKISVSNPP 337
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
AAP32736 PRELIMINARY; PRT; 337 AA.
AC AAP32736;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE G protein-coupled receptor 80.
GN GPR80.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15001573;
RA Inbe H., Watanabe S., Miyawaki M., Tanabe E., Encinas J.A.;
RT "Identification and characterization of a cell-surface receptor,
RT P2Y15, for AMP and adenosine";
RL J. Biol. Chem. 279:19790-19799(2004).
DR EMBL; AY191367; AAP32736.1; -.
SQ SEQUENCE 337 AA; 38377 MW; 9899E80DE0531CB9 CRC64;

Query Match 84.0%; Score 1487; DB 2; Length 337;
Best Local Similarity 85.8%; Pred. No. 5.5e-93;
Matches 289; Conservative 10; Mismatches 38; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGFGNNAVISTYIF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MIEPLDSPASDSDFLDYITALENCTDEQISFKQYLPVIYGIIFLVGFGNNAVISTYIF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 KMRPWKSSIIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFRFSPHFNYLSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 KMRPWKSSIIIMNLALTDLTYLTSPLFIHYASGENWIFGDMCKFRFSPHFNYLSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNRTNR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 ILFLTCSLFRVIVIIHPMSCFSIQKTRWAVVACAGWVISLVAVMPMTFLTSTNRTNR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 SACLDLTSSDELTIKWYNLIITATTCFLPLVIVTLCYTTIITLTHGLQDSCLOKAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 SACLDLTSSDDLTIKWYNLIITATTCFLPLVIVTLCYTTIITLTHGPRTHSCFKOKAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 RLTIILLAFYVCFPLPFHILVRIRIESRLLSISCSIESIENIHEAYIVSRPLAALNTFGNLL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 RLTIILLAFYVCFPLPFHILVRIRIESRLLSISCSIESIENIHEAYIVSRPLAALNTFGNLL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 LVVVSDNFQQAQVCSVTRCKVSGNLEQAQKISVSNPP 337
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 LVVVSNPFQQAQVCSVTRCKVSGNLEQAQKISVSNPP 337
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 102 LTPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSLFTCSAHRYSGVVVPLKSLG 161  
 QY 144 IHKTRCAVACAVVWLIISAVIPMTFLTSTNTRNS-ACLDLTSSDELNTIKWNLL 202  
 Db 162 RLKKNAICISVWLVVILSPILFYSGTGVRRNKTTTCYDTSDEYLSFYISMT 221  
 QY 203 TATTFCLPLVIVTLCYTTIHTLTHGLQDSCILKQKARLTILLIAFYVCLPFIHLRV 262  
 Db 222 TVAMFCVPLVILGCVGLIVRALIVKLDNSPLRRKSIYLVILVTFAVSIPIHVMKT 281  
 QY 263 IRIEISRL--LSISCSIEHQIHEIVSRPLAALTFGNLLYVVVDNFQOAVCSTVR 318  
 Db 282 MNLRLARLDQTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRLSRATR 340

## RESULT 13

P2YR CHICK  
 ID P2YR CHICK STANDARD; PRT; 362 AA.  
 AC P34996;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).  
 GN Name=P2Y1;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1] ID=9031;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93285340; PubMed=8508924;  
 RA Webb T.E., Simon J., Krishak B.J., Bateson A.N., Smart T.G.,  
 RA King B.F., Burnstock G., Barnard E.A.;  
 RT "Cloning and functional expression of a brain G-protein-coupled ATP  
 receptor.";  
 RL FEBS Lett. 324:219-225(1993).  
 RN [2]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=97026278; PubMed=8872457;  
 RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;  
 RT "Modelling the P2Y purinoceptor using rhodopsin as template.";  
 RL Drug Des. Discov. 13:133-140(1995).  
 CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as  
 ATP and ADP. Seems to mediate its action via a pertussis toxin  
 insensitive G-protein, probably belonging to the Gq family that  
 activate a phosphatidylinositol-calcium second messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Brain, spinal cord, gastrointestinal tract,  
 spleen and leg muscle. Is not detected in the heart, liver,  
 stomach, lung and kidney.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; X73268; CAA51716.1; -.  
 CC PIR; S33733; S33733.  
 CC PDB; 1DDD; Model; 1-39-71, 2-75-104, 3-113-139, 4-152-180, 5-203-233, 6-248-277, 7-  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC InterPro; IPR000142; P2Y\_purinocptor.  
 CC InterPro; IPR002286; P2Y\_purinocptor.  
 CC Pfam; PF00001; 7tm1.1;  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PROSITE; PS00237; G\_PROTEIN\_RCEP\_F1\_1; 1.  
 CC PROSITE; PS00262; G\_PROTEIN\_RCEP\_F1\_2; 1.  
 KW 3D-structure; G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 41 Extracellular (Potential).  
 FT TRANSMEM 42 63 1 (Potential).  
 FT DOMAIN 64 76 Cytoplasmic (Potential).  
 FT TRANSMEM 77 98 2 (Potential).  
 FT DOMAIN 99 115 Extracellular (Potential).  
 FT TRANSMEM 116 136 3 (Potential).  
 FT DOMAIN 137 155 Cytoplasmic (Potential).  
 FT TRANSMEM 156 177 4 (Potential).  
 FT DOMAIN 178 207 Extracellular (Potential).  
 FT TRANSMEM 208 227 5 (Potential).  
 FT DOMAIN 228 254 Cytoplasmic (Potential).  
 FT TRANSMEM 255 274 6 (Potential).  
 FT DOMAIN 275 292 Extracellular (Potential).  
 FT TRANSMEM 293 317 7 (Potential).  
 FT DOMAIN 318 362 Cytoplasmic (Potential).  
 FT DISULFID 113 191 By similarity.  
 FT CARBOHYD 11 11 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 26 26 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 102 102 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 186 186 N-linked (GlcNAc. .) (Potential).  
 FT HELIX 42 69  
 FT HELIX 77 102  
 FT HELIX 115 137  
 FT HELIX 154 178  
 FT HELIX 205 231  
 FT HELIX 250 275  
 FT HELIX 290 305  
 FT TURN 306 307  
 FT HELIX 308 320  
 SQ SEQUENCE 362 AA; 41194 MW; A806C88FB9514761 CRC64;  
 Query Match 31.9%; Score 565.5; DB 1; Length 362;  
 Best Local Similarity 35.0%; Pred. No. 1.4e-30;  
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;  
 QY 1 MNEPDIYLANASDFDYAA---AFGN---CTDENIPLKMHVLPVYIGIIFLNGPFGNAV 53  
 Db 1 MTEALISALNGTQPELLAGWAGNATKSLTKGTFQFYLPVYILVITGFLGNSV 60  
 QY 54 VISTYIFQMRPWKSTIIMNLACTDLYLTLPLIHYASGENWIFGDFMCKFIRFSF 113  
 Db 61 AIWPFVFMHWPMSGISVYMFNLALADFLYVLTLPALIFVYFNKTDWIFGDMCKLQRF 120  
 QY 114 HFNLYSSILFTCSIFHYCVIIHPMSCFSIHKTRCAVACAVVWLIISAVIPMTFLI- 172  
 Db 121 HVNLKGSILFTCSVHRVTGVVHPLKSLGRKKNVYVSVLWVAVIAPIFLFYSG 180  
 QY 173 TSTNTRNSACLDTSSDELNTIKWNLLIATATPCLPLVITLCYTTIHTLTHGLQTD 232  
 Db 181 TGVRNKTITCYDTADEVLSYFVYSNCTTFWECIPFVILGCVGLIVKALIVKLDLN 240  
 QY 233 SCLQKARLTILLIAPYVCLPFIHLRVIRISRL--LSISCSIEHQIHEAVISRP 289  
 Db 241 SPLRRKSIYLVILTVFAVSILPFIHVMKTLNRLARLDQTPMCAFNDKVVATYQVTRG 300  
 QY 290 LAALNTFNLLYVVVDNFQOAVCSTVR 318  
 Db 301 LASLNSCVDPILYFLAGDTFRRLSRATR 329

## RESULT 14

P2YR MELGA  
 ID P2YR MELGA STANDARD; PRT; 362 AA.  
 AC P49652;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1  
 DE orphan receptor).  
 GN Name=P2Y1;  
 OS Meleagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.

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OX NCBI_TaxID=9103;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94335907; PubMed=8058061;
RA Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
RT "Expression of a cloned P2Y purinergic receptor that couples to
RT phospholipase C.";
RL Mol. Pharmacol. 46:8-14 (1994).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=9240460;
RX Li Q., Schachter J.B., Harden T.K., Nicholas R.A.;
RT "The 6H1 orphan receptor, claimed to be the P2Y5 receptor, does not
RT mediate nucleotide-promoted second messenger responses.";
RL Biochem. Biophys. Res. Commun. 236:455-460 (1997).
CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. Seems to mediate its action via a pertussis toxin
CC insensitive G-protein, probably belonging to the Gq family that
CC activate a phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Mainly found in blood, brain, and lung. To a
CC lesser extent in stomach, gut and skeletal muscle.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
EMBL; U09842; AAA18784.1; -.
DR AF012103; AAB65428.1; -.
DR HGSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000142; P2Y_purinocptor.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP Fl_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 41 Extracellular (Potential).
FT TRANSMEM 42 73 1 (Potential).
FT DOMAIN 64 76 2 (Potential).
FT TRANSMEM 77 98 3 (Potential).
FT DOMAIN 116 136 4 (Potential).
FT TRANSMEM 137 155 5 (Potential).
FT TRANSMEM 156 177 6 (Potential).
FT DOMAIN 178 207 7 (Potential).
FT TRANSMEM 208 227 8 (Potential).
FT DOMAIN 228 254 9 (Potential).
FT TRANSMEM 255 274 10 (Potential).
FT DOMAIN 275 292 11 (Potential).
FT TRANSMEM 293 317 12 (Potential).
FT DOMAIN 318 362 13 (Potential).
FT DISULFID 113 191 14 (Potential).
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 362 AA; 41180 MW; 3E128AB9B64349C CRC64;
Query Match 31.9%; Score 565.5; DB 1; Length 362;
Best Local Similarity 35.0%; Pred. No. 1.4e-30;
Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;
QY 1 MNEPLDLYANASDFPDYAR--AFGN---CTDENILPKMHVLPVYIGIIFLVGFPGNAY 53
DB 1 MTEALISAALNGTQPELLAGGWAAGNASTKSLTKTGTFQFYLPTVYILVFTGFLGNSV 60

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QY 54 VISTYIFKORPKWSSTIIMLNLACTDLYLTSLPFLIHYYASGENWIFGDMCKFIKFSF 113
DB 61 AIWMFVHMRPWSGISVYMFENLADFLYVLTLPALIFYFYNTKDMIFGDMCKLQRFIF 120
QY 114 HFNLYSILFLTCFSIFRYCVIIHPMSCFSIHTRCAVACAVVWISLVAVIPMTFLI- 172
DB 121 HVNLYSILFLTCISVHRVTGVVHPLKSLGRLKKQNAVYVSSLVWALVAVIAPILFYS 180
QY 173 TSTNRTNSACLDITSSDELNTIKWYNLILATATTCCLPLVITLCYTTIITHTHGLQTD 232
DB 181 TGVRRNKTIITCYDTTADDEYLRVYFVSMCTVMFCIPFVILGCGYGLIYKLDLN 240
QY 233 SCLQKARRITILLALAFYVCFPLPHILIRVIRIESRL---LSISCSSTENQHEAYIYSRP 289
DB 241 SPLRKSILYVILVITVFAVSYPFLPHWKTNLRLARLDFTQPMCAFNKVKYATYQVTRG 300
QY 290 LAALNTFENLLVYVSDNFQQAQVSVR 318
DB 301 LASINSCVDPLILYPLAGDTFRRLSRATR 329
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AC P49651;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE P2Y purinocptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN Name=P2Y1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Insulinoma;
RX MEDLINE=95298025; PubMed=7779087;
RA Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT "Cloning of rat and mouse P2Y purinocptors."
RL Biochem. Biophys. Res. Commun. 211:211-218 (1995).
CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. In pancreatic islets, may mediate some of the effects
CC of extracellular ATP on insulin secretion.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in muscle, heart, liver, kidney,
CC lung, brain, spleen, but not in testis.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
EMBL; U22830; AAA91303.1; -.
DR HGSP; P34996; 1DDD.
DR RGD; 3242; P2Y1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000142; P2Y_purinocptor.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 52 Extracellular (Potential).
FT TRANSMEM 53 74 1 (Potential).
FT DOMAIN 75 87 2 (Potential).
FT TRANSMEM 88 109 2 (Potential).

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| FT  | TRANSMEM | 127   | 147 | 3 (Potential).                    |
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| FT  | TRANSMEM | 167   | 188 | 4 (Potential).                    |
| FT  | DOMAIN   | 189   | 218 | Extracellular (Potential).        |
| FT  | TRANSMEM | 219   | 238 | 5 (Potential).                    |
| FT  | DOMAIN   | 239   | 265 | Cytoplasmic (Potential).          |
| FT  | TRANSMEM | 266   | 285 | 6 (Potential).                    |
| FT  | DOMAIN   | 286   | 303 | Extracellular (Potential).        |
| FT  | TRANSMEM | 304   | 328 | 7 (Potential).                    |
| FT  | DOMAIN   | 329   | 373 | Cytoplasmic (Potential).          |
| FT  | DISULFID | 124   | 202 | By similarity.                    |
| FT  | CARBOHYD | 11  | 11  | N-linked (GlcNAc. .) (Potential). |
| FT  | CARBOHYD | 27  | 27  | N-linked (GlcNAc. .) (Potential). |
| FT  | CARBOHYD | 113   | 113 | N-linked (GlcNAc. .) (Potential). |
| FT  | CARBOHYD | 197   | 197 | N-linked (GlcNAc. .) (Potential). |
| SQ  | SEQUENCE | 373 AA; 42321 MW; 6DDF676287B5E648 CRC64;                   |     |                                   |
| Query Match 31.9%; Score 565; DB 1; Length 373;                 |          |   |     |                                   |
| Best Local Similarity 36.8%; Pred. No. 1.5e-30;                 |          |   |     |                                   |
| Matches 107; Conservative 67; Mismatches 113; Indels 4; Gaps 2; |          |   |     |                                   |
| Qy  | 32       | KMHYLPVYIGIFLYFPCNAVVISYIFKMPKSSIIIMLNACTDILLYLTSLPFLIH     | 91  |                                   |
| Db  | 50       | QFYLPVAVIILVFIIGFLGNSVAIMFVFMKPSGISVYMENLALADFLYVLTLPALIF   | 109 |                                   |
| Qy  | 92       | YYASGENWIFGDMCKFIRFGFHNLYSILFLTCFSIFRYCVIIHPMCSFSIHKTRCAV   | 151 |                                   |
| Db  | 110      | YYFNKTDWIFGDVMCKLQRFIFHNLYSILFLTCISAHRYSGVVPKSLGRLKKKNAI    | 169 |                                   |
| Qy  | 152      | VACAVVWIIISLVAVIPMTFLTITSTNTRNS-ACDLTSSDELNTIKWYNLIITATTCLP | 210 |                                   |
| Db  | 170      | YVSVLWLVVVAISPILFYSGTGIRKNKTVTCYDSTSDVLSRVFYISMCTTVAMFCIP   | 229 |                                   |
| Qy  | 211      | LVIVTLCYTTIHTHGLQTDSCIKQKARLTILLILAFVYCFPLPHILRVIRIESRL-    | 269 |                                   |
| Db  | 230      | LVILGCGYGLIVRALIYKLDNSPLRRKSIYLVIIVLTVPFVAVSYIPFHVMTMNLRLD  | 289 |                                   |
| Qy  | 270      | --LSISCSIQIHEAYIVSRPLAALNTFGNLLLVVVVDNFQOAVCVSTR            | 318 |                                   |
| Db  | 290      | FQTEPCDFNDRVATYQVTRGLASLNSCDVPILYFLAGDTFRRLSRATR            | 340 |                                   |

Search completed: October 29, 2004, 15:04:33  
Job time : 194 secs

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# OM protein - protein search, using sw model

Run on: October 29, 2004, 14:50:53 ; Search time 141 Seconds  
(without alignments)  
774.899 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVSGNLEQAKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 1          | 1771  | 100.0       | 337    | 9  | US-09-943-798-4   |
| 2          | 1771  | 100.0       | 337    | 10 | US-09-885-453-1   |
| 3          | 1771  | 100.0       | 337    | 14 | US-10-023-775B-2  |
| 4          | 1771  | 100.0       | 337    | 14 | US-10-270-144-2   |
| 5          | 1771  | 100.0       | 337    | 14 | US-10-188-405-8   |
| 6          | 1771  | 100.0       | 337    | 14 | US-10-079-384-14  |
| 7          | 1771  | 100.0       | 337    | 14 | US-10-278-141-2   |
| 8          | 1771  | 100.0       | 337    | 14 | US-10-017-161-526 |
| 9          | 1771  | 100.0       | 337    | 14 | US-10-010-568-2   |
| 10         | 1771  | 100.0       | 337    | 14 | US-10-321-807-28  |
| 11         | 1771  | 100.0       | 337    | 14 | US-10-296-081-2   |
| 12         | 1771  | 100.0       | 337    | 14 | US-10-375-157-2   |
| 13         | 1771  | 100.0       | 337    | 14 | US-10-292-798-464 |

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|----|--------|-------|-----|----|--------------------|-------------------|
| 14 | 1771   | 100.0 | 337 | 14 | US-10-023-634-6    | Sequence 6, Appli |
| 15 | 1771   | 100.0 | 337 | 14 | US-10-023-634-57   | Sequence 57, Appl |
| 16 | 1771   | 100.0 | 337 | 15 | US-10-055-569A-8   | Sequence 8, Appli |
| 17 | 1771   | 100.0 | 337 | 15 | US-10-344-728-2    | Sequence 2, Appli |
| 18 | 1771   | 100.0 | 337 | 15 | US-10-343-650A-14  | Sequence 14, Appl |
| 19 | 1771   | 100.0 | 337 | 16 | US-10-321-807-28   | Sequence 28, Appl |
| 20 | 1771   | 100.0 | 337 | 16 | US-10-763-854-2    | Sequence 2, Appli |
| 21 | 1771   | 100.0 | 337 | 16 | US-10-314-048A-28  | Sequence 28, Appl |
| 22 | 1771   | 100.0 | 337 | 17 | US-10-775-965-111  | Sequence 11, App  |
| 23 | 1764   | 99.6  | 337 | 14 | US-10-225-567A-647 | Sequence 647, App |
| 24 | 1764   | 99.6  | 337 | 14 | US-10-400-991-16   | Sequence 16, Appl |
| 25 | 1602.5 | 90.5  | 336 | 10 | US-09-782-974C-86  | Sequence 86, Appl |
| 26 | 1444   | 81.5  | 276 | 9  | US-09-943-798-2    | Sequence 2, Appli |
| 27 | 881.5  | 49.8  | 179 | 15 | US-10-276-774-1452 | Sequence 1452, Ap |
| 28 | 831.5  | 47.0  | 192 | 10 | US-09-782-974C-60  | Sequence 60, Appl |
| 29 | 575    | 32.5  | 299 | 14 | US-10-270-144-4    | Sequence 4, Appli |
| 30 | 575    | 32.5  | 373 | 14 | US-10-010-568-5    | Sequence 5, Appli |
| 31 | 575    | 32.5  | 373 | 14 | US-10-375-157-5    | Sequence 5, Appli |
| 32 | 575    | 32.5  | 373 | 14 | US-10-023-634-58   | Sequence 58, Appl |
| 33 | 575    | 32.5  | 373 | 15 | US-10-055-569A-50  | Sequence 50, Appl |
| 34 | 567    | 32.0  | 373 | 10 | US-09-745-842-14   | Sequence 14, Appl |
| 35 | 567    | 32.0  | 373 | 14 | US-10-092-135-6    | Sequence 6, Appli |
| 36 | 567    | 32.0  | 373 | 14 | US-10-225-567A-219 | Sequence 219, App |
| 37 | 567    | 32.0  | 373 | 14 | US-10-010-568-8    | Sequence 8, Appli |
| 38 | 567    | 32.0  | 373 | 14 | US-10-375-157-8    | Sequence 59, Appl |
| 39 | 567    | 32.0  | 373 | 14 | US-10-023-634-59   | Sequence 51, Appl |
| 40 | 567    | 32.0  | 373 | 15 | US-10-055-569A-51  | Sequence 6, Appli |
| 41 | 567    | 32.0  | 373 | 15 | US-10-344-728-6    | Sequence 28, Appl |
| 42 | 565.5  | 31.9  | 362 | 10 | US-09-779-679-28   | Sequence 3, Appli |
| 43 | 565.5  | 31.9  | 362 | 10 | US-09-991-225-3    | Sequence 4, Appli |
| 44 | 565.5  | 31.9  | 362 | 10 | US-09-991-225-4    | Sequence 3, Appli |
| 45 | 565.5  | 31.9  | 362 | 14 | US-10-092-135-3    |                   |

## ALIGNMENTS

RESULT 1  
US-09-943-798-4  
; Sequence 4, Application US/09943798  
; Patent No. US20020065215A1  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Group Limited  
; TITLE OF INVENTION: Polypeptide  
; FILE REFERENCE: QG1021  
; CURRENT APPLICATION NUMBER: US/09/943,798  
; CURRENT FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-943-798-4

|                       |                 |                      |            |   |
|-----------------------|-----------------|----------------------|------------|---|
| Query Match           | 100.0%          | Score 1771:          | DB 9:      | Length 337;                             |
| Best Local Similarity | 100.0%          | Pred. No. 3.5e-156;  |            |   |
| Matches 337;          | Conservative 0; | Mismatches 0;        | Indels 0;  | Gaps 0;                                 |
| QY                    | 1               | MNEPLDYLANASDFPDYAAA | FGNCTDENIP | PLKMHYLPVIYIGIIFLVGPGNAVISTVIF 60       |
| Db                    | 1               | MNEPLDYLANASDFPDYAAA | FGNCTDENIP | PLKMHYLPVIYIGIIFLVGPGNAVISTVIF 60       |
| QY                    | 61              | KMRPKWSSTIIMLNACTD   | LLYLSLP    | PLPIHYASGENWIFGDFMCKIRFSFHNLYSS 120     |
| Db                    | 61              | KMRPKWSSTIIMLNACTD   | LLYLSLP    | PLPIHYASGENWIFGDFMCKIRFSFHNLYSS 120     |
| QY                    | 121             | ILFLTCFSIFRYCVIIHP   | MSCFS      | HKTKCAVACAVVMIISLVAVIPMTLETSTNTRNR 180  |
| Db                    | 121             | ILFLTCFSIFRYCVIIHP   | MSCFS      | HKTKCAVACAVVMIISLVAVIPMTLETSTNTRNR 180  |
| QY                    | 181             | SACDLTSSDELNTIKWYN   | LIITAT     | TFCLPVIIVTLCTVTTIHTLTHGLQDSCILKOKAR 240 |
| Db                    | 181             | SACDLTSSDELNTIKWYN   | LIITAT     | TFCLPVIIVTLCTVTTIHTLTHGLQDSCILKOKAR 240 |

Db 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTLILLAFVVCFLPHILRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Db 241 RLTLILLAFVVCFLPHILRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGVSTVRCVKVSGNLEQAKKISYSNNP 337  
Db 301 LYVVSDNFQAVGVSTVRCVKVSGNLEQAKKISYSNNP 337  
RESULT 2  
US-09-885-453-1  
; Sequence 1, Application US/09885453  
; Publication No. US20030088080A1  
; GENERAL INFORMATION:  
; APPLICANT: Commun1, Didier  
; TITLE OF INVENTION: RECEPTOR GPCRxl0  
; FILE REFERENCE: 9409/2082  
; CURRENT APPLICATION NUMBER: US/09/885,453  
; CURRENT FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: US 09/885,453  
; PRIOR FILING DATE: 2001-06-21  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: amino acid sequence GPCRxl0  
; LOCATION: (1)..(337)  
; OTHER INFORMATION: GPCRxl0 amino acid sequence  
US-09-885-453-1

Query Match 100.0%; Score 1771; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120  
Db 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120  
QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLITSTNTR 180  
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLITSTNTR 180  
QY 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240  
Db 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTLILLAFVVCFLPHILRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Db 241 RLTLILLAFVVCFLPHILRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGVSTVRCVKVSGNLEQAKKISYSNNP 337  
Db 301 LYVVSDNFQAVGVSTVRCVKVSGNLEQAKKISYSNNP 337

RESULT 3  
US-10-023-775B-2  
; Sequence 2, Application US/10023775B  
; Publication No. US20030022828A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc. (GB) only  
; APPLICANT: Pfizer Inc. (US, JP, EB except GB)  
; APPLICANT: Fidock, Mark David  
; TITLE OF INVENTION: No. US20030022828A1el Polypeptide

; FILE REFERENCE: PC10959AGPR  
; CURRENT APPLICATION NUMBER: US/10/023,775B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: GB 0030854.4  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/260,590  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: US 60/296,660  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: GB 0111031.1  
; PRIOR FILING DATE: 2001-05-04  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-023-775B-2

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120  
Db 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120  
QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLITSTNTR 180  
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLITSTNTR 180  
QY 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240  
Db 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTLILLAFVVCFLPHILRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Db 241 RLTLILLAFVVCFLPHILRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGVSTVRCVKVSGNLEQAKKISYSNNP 337  
Db 301 LYVVSDNFQAVGVSTVRCVKVSGNLEQAKKISYSNNP 337

RESULT 4  
US-10-270-144-2  
; Sequence 2, Application US/10270144  
; Publication No. US20030049790A1  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL000750CON  
; CURRENT APPLICATION NUMBER: US/10/270,144  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/205,196  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Human  
US-10-270-144-2

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFENLYSS 120  
DB 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFENLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNRTNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNRTNR 180  
QY 181 SACLDLTSSDELTNIKWNLLITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACLDLTSSDELTNIKWNLLITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

## RESULT 5

US-10-188-405-8

; Sequence 8, Application US/10188405

; Publication No. US20030082585A1

; GENERAL INFORMATION:

; APPLICANT: Tian, Kang

; APPLICANT: Dai, Kang

; APPLICANT: Chen, Jin-Long

; APPLICANT: Zhao, Jiagang

; APPLICANT: Cutler, Gene

; APPLICANT: Tularik Inc.

; TITLE OF INVENTION: No. US20030082585A1el Receptors

; FILE REFERENCE: 018781-00841005

; CURRENT APPLICATION NUMBER: US/10/188,405

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US 60/302,800

; PRIOR FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 8

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human TGR164

US-10-188-405-8

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFENLYSS 120  
DB 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFENLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNRTNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNRTNR 180  
QY 181 SACLDLTSSDELTNIKWNLLITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACLDLTSSDELTNIKWNLLITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKQKAR 240

QY 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

## RESULT 6

US-10-079-384-14

; Sequence 14, Application US/10079384

; Publication No. US20030108986A1

; GENERAL INFORMATION:

; APPLICANT: Communi, Didier

; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: 9409/2132

; CURRENT APPLICATION NUMBER: US/10/079,384

; CURRENT FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 09/885,453

; PRIOR FILING DATE: 2001-06-20

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 14

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-079-384-14

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFENLYSS 120  
DB 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFENLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNRTNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNRTNR 180  
QY 181 SACLDLTSSDELTNIKWNLLITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACLDLTSSDELTNIKWNLLITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

## RESULT 7

US-10-278-141-2

; Sequence 2, Application US/10278141

; Publication No. US20030138818A1

; GENERAL INFORMATION:

; APPLICANT: PATTERSON, Chandra

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: THORNTON, Michael

; APPLICANT: LU, Yan

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: GRAUL, Richard

; APPLICANT: KHAN, Farrah A.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: WALIA, Narinder K.

; APPLICANT: NGUYEN, Dannie B.

; APPLICANT: YUE, Henry  
; APPLICANT: HAFALIA, April  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: LAL, Preeti  
; APPLICANT: REDDY, Roopa  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AU-YOUNG, Janice  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0096 USA  
; CURRENT APPLICATION NUMBER: US/10/278,141  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR FILING DATE: 60/208,834  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR FILING DATE: 60/207,566  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR FILING DATE: 60/205,628  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR FILING DATE: 60/208,861  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR FILING DATE: 60/206,222  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030138818A1 6575963CD1  
US-10-278-141-2

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60  
Qy 61 KMRPWKSTTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDFMCKFIKPSFHNLYSS 120  
Db 61 KMRPWKSTTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDFMCKFIKPSFHNLYSS 120  
Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAIIPMTFLITSTNTR 180  
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAIIPMTFLITSTNTR 180  
Qy 181 SACLDLTSSDELNTIKWYNILITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKOKAR 240  
Db 181 SACLDLTSSDELNTIKWYNILITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKOKAR 240  
Qy 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Db 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Qy 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Qy 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337  
Db 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 8  
US-10-017-161-526  
; Sequence 526, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 526  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-526

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60  
Qy 61 KMRPWKSTTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDFMCKFIKPSFHNLYSS 120  
Db 61 KMRPWKSTTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDFMCKFIKPSFHNLYSS 120  
Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAIIPMTFLITSTNTR 180  
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAIIPMTFLITSTNTR 180  
Qy 181 SACLDLTSSDELNTIKWYNILITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKOKAR 240  
Db 181 SACLDLTSSDELNTIKWYNILITATTCPLPVIIVTLCTYIIHTLTHGLQDSCCLKOKAR 240  
Qy 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Db 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
Qy 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337  
Db 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 9  
US-10-010-568-2  
; Sequence 2, Application US/10010568  
; Publication No. US20030157598A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWMY23, EXPRESSED HIC  
; FILE REFERENCE: D0077 NP  
; CURRENT APPLICATION NUMBER: US/10/010,568  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/251,926  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/269,795  
; PRIOR FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-010-568-2

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60



QY 61 KMRPWKSTIIIMLNACTDLYLTSLPFLIHYASGENWIFGDFMCKFIRFSFHNLYSS 120  
Db 61 KMRPWKSTIIIMLNACTDLYLTSLPFLIHYASGENWIFGDFMCKFIRFSFHNLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVWMIISLVAVIPMTFLTSTNRTNR 180  
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVWMIISLVAVIPMTFLTSTNRTNR 180  
QY 181 SACLDLTSSDELNTIKWYNLILTATTFCPLPVIVITVLCVYTIHTLTHGLQDSCCLKQKAR 240  
Db 181 SACLDLTSSDELNTIKWYNLILTATTFCPLPVIVITVLCVYTIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFYVCFPHILVRIRIESRLLSIENQIHEAYIVSRPLAALNTFGNLL 300  
Db 241 RLTIILLAFYVCFPHILVRIRIESRLLSIENQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337  
Db 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 10  
US-10-321-807-28  
; Sequence 28, Application US/10321807  
; Publication No. US20030166148A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Rupong T.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Lowitz, Kevin P.  
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN0086  
; CURRENT APPLICATION NUMBER: US/10/321,807  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US/09/714,008  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,088  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,099  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,369  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/171,902  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/171,901  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/171,900  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/181,749  
; PRIOR FILING DATE: 2000-02-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-321-807-28

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNEPLDYLANASDPDYAAAFNCNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNCNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPWKSTIIIMLNACTDLYLTSLPFLIHYASGENWIFGDFMCKFIRFSFHNLYSS 120

Db 61 KMRPWKSTIIIMLNACTDLYLTSLPFLIHYASGENWIFGDFMCKFIRFSFHNLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVWMIISLVAVIPMTFLTSTNRTNR 180  
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVWMIISLVAVIPMTFLTSTNRTNR 180  
QY 181 SACLDLTSSDELNTIKWYNLILTATTFCPLPVIVITVLCVYTIHTLTHGLQDSCCLKQKAR 240  
Db 181 SACLDLTSSDELNTIKWYNLILTATTFCPLPVIVITVLCVYTIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFYVCFPHILVRIRIESRLLSIENQIHEAYIVSRPLAALNTFGNLL 300  
Db 241 RLTIILLAFYVCFPHILVRIRIESRLLSIENQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337  
Db 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 11  
US-10-296-081-2  
; Sequence 2, Application US/10296081  
; Publication No. US20030220477A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: THORNTON, Michael  
; APPLICANT: LU, Yan  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: GRAUL, Richard  
; APPLICANT: KHAN, Farrah A.  
; APPLICANT: GANDHI, Aameena R.  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: NGUYEN, Daniel B.  
; APPLICANT: YUE, Henry  
; APPLICANT: HAPALIA, April  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: LAL, Preeti  
; APPLICANT: REDDY, Roopa  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AU-YOUNG, Janice  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0096 PCT  
; CURRENT APPLICATION NUMBER: US/10/296,081  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208,861  
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20030220477A1 6575963CD1  
US-10-296-081-2

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNEPLDYLANASDPDYAAAFNCNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
Db 1 MNEPLDYLANASDPDYAAAFNCNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPWKSTIIIMLNACTDLYLTSLPFLIHYASGENWIFGDFMCKFIRFSFHNLYSS 120  
Db 61 KMRPWKSTIIIMLNACTDLYLTSLPFLIHYASGENWIFGDFMCKFIRFSFHNLYSS 120

QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180  
QY 181 SACDLTSSDELNTIKWYNLILATTFCLPLVIVTLVCTTIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACDLTSSDELNTIKWYNLILATTFCLPLVIVTLVCTTIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

## RESULT 12

US-10-375-157-2  
; Sequence 2, Application US/10375157  
; Publication No. US20030224458A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY23, EXPRESSED  
; FILE REFERENCE: D0077A CIP  
; CURRENT APPLICATION NUMBER: US/10/375,157  
; PRIOR FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: US 60/251,926  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 10/010,568  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/269,795  
; PRIOR FILING DATE: 2001-02-14  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-375-157-2

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120  
DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180  
QY 181 SACDLTSSDELNTIKWYNLILATTFCLPLVIVTLVCTTIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACDLTSSDELNTIKWYNLILATTFCLPLVIVTLVCTTIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

## RESULT 13

US-10-292-798-464

; Sequence 464, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 464  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-464

Query Match 100.0%; Score 1771; DB 14; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.5e-156;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120  
DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180  
QY 181 SACDLTSSDELNTIKWYNLILATTFCLPLVIVTLVCTTIIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACDLTSSDELNTIKWYNLILATTFCLPLVIVTLVCTTIIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

## RESULT 14

US-10-023-634-6  
; Sequence 6, Application US/10023634  
; Publication No. US20030236389A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Colman, Steven D  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Ballinger, Robert A  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Li, Li  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Zernusen, Bryan D  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Edinger, Shlomit R

```
; APPLICANT: Gangolli, Esba A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-634-6

Query Match      100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFDYAAAFGNCCTDENIPLKMHYLPVIYGIIFLVGFGNAVISTYIF 60
Db 1 MNEPLDYLANASDFDYAAAFGNCCTDENIPLKMHYLPVIYGIIFLVGFGNAVISTYIF 60
QY 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFNLVSS 120
Db 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFNLVSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFIIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFIIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
QY 181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCTYTTIIHTLTHGLQDSCCLKQKAR 240
Db 181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCTYTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTILLAFYVCFLPFHILRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
Db 241 RLTILLAFYVCFLPFHILRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
QY 301 LVVVSDNFQQAVCSIVRCKVSGNLEQAKKISYSNNP 337
Db 301 LVVVSDNFQQAVCSIVRCKVSGNLEQAKKISYSNNP 337
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RESULT 15

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US-10-023-634-57
; Sequence 57, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
```

```
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gangolli, Esba A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-634-57

Query Match      100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFDYAAAFGNCCTDENIPLKMHYLPVIYGIIFLVGFGNAVISTYIF 60
Db 1 MNEPLDYLANASDFDYAAAFGNCCTDENIPLKMHYLPVIYGIIFLVGFGNAVISTYIF 60
QY 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFNLVSS 120
Db 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGENWIFGDMCKFIRFSHFNLVSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFIIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFIIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
QY 181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCTYTTIIHTLTHGLQDSCCLKQKAR 240
Db 181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCTYTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTILLAFYVCFLPFHILRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
Db 241 RLTILLAFYVCFLPFHILRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
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Db 241 RLTI LLLAFYVCF LPHILRVIRIESLLSISCS IENQIHEAVI VSRPLAALNTFGNLL 300  
QY 301 LYVVVSDNFQOAVCGSTVRCKVSGNLEQAKKISYNNP 337  
Db 301 LYVVVSDNFQOAVCGSTVRCKVSGNLEQAKKISYNNP 337

Search completed: October 29, 2004, 15:07:49  
Job time : 144 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 14:13:22 ; Search time 159 Seconds  
(without alignments)

760.326 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANRDPDYAAA.....RCKVSGNLEQAKKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 1771  | 100.0       | 337    | 4     | Aau04375 Human G-p |
| 2          | 1771  | 100.0       | 337    | 5     | Aae16171 Human G-p |
| 3          | 1771  | 100.0       | 337    | 5     | Abg76871 Human G-p |
| 4          | 1771  | 100.0       | 337    | 5     | Abb83819 Human P2Y |
| 5          | 1771  | 100.0       | 337    | 5     | Abg70271 Human Pur |
| 6          | 1771  | 100.0       | 337    | 5     | Aao14027 Human P2Y |
| 7          | 1771  | 100.0       | 337    | 5     | Aau77600 Human P2Y |
| 8          | 1771  | 100.0       | 337    | 5     | Aae21803 Human AXO |
| 9          | 1771  | 100.0       | 337    | 5     | Abp95602 Human GPC |
| 10         | 1771  | 100.0       | 337    | 5     | Aao15399 Human G-p |
| 11         | 1771  | 100.0       | 337    | 5     | Abb79438 Human P2Y |
| 12         | 1771  | 100.0       | 337    | 5     | Abb81902 Human G-p |
| 13         | 1771  | 100.0       | 337    | 5     | Abg70287 Human nov |
| 14         | 1771  | 100.0       | 337    | 6     | Abp71377 Human TGR |
| 15         | 1771  | 100.0       | 337    | 7     | Adc26010 Human Pur |
| 16         | 1771  | 100.0       | 337    | 7     | Adc86011 Human GPC |
| 17         | 1771  | 100.0       | 337    | 7     | Abw00808 Human GPC |
| 18         | 1771  | 100.0       | 337    | 7     | Adl96474 Human G-p |
| 19         | 1771  | 100.0       | 337    | 8     | Adm10574 Human P2Y |
| 20         | 1771  | 100.0       | 337    | 8     | Ado29442 Human GPC |
| 21         | 1771  | 100.0       | 337    | 6     | Aae33315 Human TAR |
| 22         | 1771  | 100.0       | 345    | 6     | Aae33318 Human TAR |
| 23         | 1771  | 100.0       | 363    | 6     | Aae33317 Human TAR |
| 24         | 1771  | 100.0       | 577    | 7     | Adf70488 Orphan re |
| 25         | 1764  | 99.6        | 337    | 4     | Aau04584 Human G-p |

## ALIGNMENTS

RESULT 1

AAU04375

ID AAU04375 standard; protein; 337 AA.

XX

AC AAU04375;

XX 23-OCT-2001 (first entry)

DT Human G-protein coupled receptor, hrUP21.

DE Human G-protein coupled receptor, hrUP21.

XX Human; G-protein coupled receptor; GPCR; hrUP21; agonist;

KW inverse agonist; lung cancer.

XX Homo sapiens.

XX WO200136471-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031509.

XX 17-NOV-1999; 99US-0166088P.

XX 17-NOV-1999; 99US-0166099P.

XX 23-DEC-1999; 99US-0171900P.

XX 23-DEC-1999; 99US-0171901P.

XX 11-FEB-2000; 2000US-0181749P.

XX 14-MAR-2000; 2000US-0189258P.

XX 10-APR-2000; 2000US-0195898P.

XX 10-APR-2000; 2000US-0195899P.

XX 28-APR-2000; 2000US-0200419P.

XX 12-MAY-2000; 2000US-0203630P.

XX 12-JUN-2000; 2000US-0210741P.

XX 21-AUG-2000; 2000US-0210982P.

XX 26-SEP-2000; 2000US-0235418P.

XX 20-SEP-2000; 2000US-0235779P.

XX 20-OCT-2000; 2000US-0242332P.

XX 20-OCT-2000; 2000US-0242343P.

XX 24-OCT-2000; 2000US-0243019P.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Lowitz KP;

XX

Abp81736 Human G p  
Adh68217 Human G-p  
Adc25998 Human pur  
Aag80971 Human nGP  
Abg93789 Human G p  
Adc12674 Human GPC  
Adm10576 Murine P2  
Ado29443 Mouse GPC  
Aae33316 Mouse TAR  
Adm10578 Rat P2Y25  
Abb83818 Human P2Y  
Aam79297 Human pro  
Abb11082 Human P2Y  
Aam80281 Human pro  
Aag80958 Human nGP  
Abg93776 Human G p  
Adf43212 Mouse P2R  
Ado29593 Mouse GPC  
Aae04389 Human P2-  
Abp54316 Human P2Y

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DR WPI; 2001-355616/37.
DR N-PSDB; AAS07948.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents.
XX
PS Claim 53; Page 114-115; 160pp; English.
XX
CC The sequence represents a human G-protein coupled receptor (GPCR),
CC hRUP21. The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR), are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer. Non-
CC endogenous version of human GPCRs are also utilized in research settings
CC and in vitro and in vivo system, incorporating GPCRs can be utilised to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased
XX
SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPPGNVAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPPGNVAVISTYIF 60
QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIRSFHFNLYSS 120
DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIRSFHFNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFISHKTKCAVACAVVWIIISLVAVIPMTFLTSTNTR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFISHKTKCAVACAVVWIIISLVAVIPMTFLTSTNTR 180
QY 181 SACLDTSSDELNTIKWNLITLTATTCFLPLIVITLCVYTIITHTLGLQDSCCLKOKAR 240
DB 181 SACLDTSSDELNTIKWNLITLTATTCFLPLIVITLCVYTIITHTLGLQDSCCLKOKAR 240
QY 241 RTILLLLAFVYCFPLPHILVIRIESRLLSISCSIQENQHEAVIVSRPLAALNTFGNLL 300
DB 241 RTILLLLAFVYCFPLPHILVIRIESRLLSISCSIQENQHEAVIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVSTVECKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQAVCVSTVECKVSGNLEQAKKISYNNP 337

RESULT 2
AAE16171
ID AAE16171 standard; protein; 337 AA.
AC AAE16171;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human G-protein coupled receptor 2 (GCRC-2) protein.
XX
KW Human; G-protein coupled receptor 2; cell proliferative disorder;
KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
KW gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
KW acquired immune deficiency syndrome; inflammatory disorder; infection;
KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
KW diabetes; obesity; osteoporosis; gene therapy; GCRC-2.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers

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FT Domain 35. .59
FT /note= "Transmembrane domain"
XX
XX WO200187937-A2.
XX
XX 22-NOV-2001.
XX
XX 17-MAY-2001; 2001WO-US016285.
XX
XX 18-MAY-2000; 2000US-0205628P.
XX 22-MAY-2000; 2000US-0206222P.
XX 25-MAY-2000; 2000US-0207566P.
XX 02-JUN-2000; 2000US-0208834P.
XX 02-JUN-2000; 2000US-0208861P.
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Patterson C, Lu DAM, Thornton M, Lu Y, Tribouley CM, Graul R;
XX Khan FA, Gandhi AR, Wallia NK, Nguyen DB, Yue H, Hafalia A;
XX Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;
XX
XX WPI; 2002-089844/12.
XX N-PSDB; AAD26370.
XX
XX Novel G-protein coupled receptors and polynucleotides useful for
XX diagnosis, treatment and prevention of disorders of cell proliferation,
XX neurological, cardiovascular, metabolic disorders and viral infections.
XX
XX Claim 1; Page 104-105; 115pp; English.
XX
XX The invention relates to human G-protein coupled receptor (GCRC)
XX polypeptides and polynucleotides. GCRC polypeptides are useful for
XX screening compounds that modulate their activity. They are useful in the
XX diagnosis, prevention and treatment of disorders which include cell
XX proliferative disorders such as arteriosclerosis, hepatitis,
XX myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
XX lymphoma; neurological disorders such as epilepsy, ischaemic
XX cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
XX Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
XX meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
XX cardiovascular disorders such as arteriovenous fistula, atherosclerotic heart
XX disease, infective endocarditis, myocardial infarction, hypertensive heart
XX disease, gastrointestinal disorders such as dysphagia, peptic oesophagitis,
XX emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
XX constipation, acquired immune deficiency syndrome (AIDS), hepatic,
XX encephalopathy; autoimmune/inflammatory disorders such as Addison's
XX disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
XX dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
XX emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
XX arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
XX fungal, parasitic, protozoal and helminthic infections and trauma;
XX metabolic disorders such as diabetes, obesity and osteoporosis; and viral
XX infections such as infection caused by viral agent classified as
XX adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are
XX useful as probes for assessing toxicity of test compounds. They are also
XX used in gene therapy. The present sequence is human G-protein coupled
XX receptor 2 (GCRC-2) protein
XX
XX Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPPGNVAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPPGNVAVISTYIF 60
QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIRSFHFNLYSS 120
DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIRSFHFNLYSS 120

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121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
181 SACLDLTSSDELTIKWYNLILTATFTFCLPLVIVTLCYTTIIHILTHGLQDSCCLKQKAR 240  
181 SACLDLTSSDELTIKWYNLILTATFTFCLPLVIVTLCYTTIIHILTHGLQDSCCLKQKAR 240  
241 RLTLILLAFVVCFLPFHILVIRIESLLISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
241 RLTLILLAFVVCFLPFHILVIRIESLLISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYNNP 337  
301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 3  
ABG76871  
ID ABG76871 standard; protein; 337 AA.  
XX AC ABG76871;  
DT 05-NOV-2002 (first entry)  
XX Human G-protein coupled receptor, HGPRBMV23.  
XX Human; G-protein coupled receptor; HGPRBMV23; receptor; GPCR; cancer;  
KW renal disorder; pulmonary disease; neural disorder; heart defect;  
KW male reproductive disorder; hyperproliferative disorder; inflammation;  
KW lymphoproliferative disease; autoimmune disease; bacterial infection;  
KW fungal infection; parasitic infection; vascular disorder; receptor;  
KW lymphatic disorder.  
XX OS Homo sapiens.  
XX WO200246414-A2.  
XX 13-JUN-2002.  
XX 07-DEC-2001; 2001WO-US046951.  
XX 07-DEC-2000; 2000US-0251926P.  
XX 14-FEB-2001; 2001US-0265795P.  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX Ramanathan C, Feder J, Nelson T, Cacace A, Barber L, Rysek R;  
XX WPI; 2002-599468/64.  
XX N-PSDB; ABS59232.  
XX New G-protein coupled receptor HGPRBMV23 polypeptide and polynucleotides,  
PT useful for diagnosing, prognosing, preventing, treating renal, immune,  
PT hyperproliferative and cardiovascular disorders and identifying  
PT modulators.  
XX Claim 33; Fig 1; 419pp; English.

The invention relates to an isolated G-protein coupled receptor (GPCR)  
protein, HGPRBMV23. The protein and its associated DNA are useful for  
preventing, treating or ameliorating a medical condition such as a renal  
disorder, a disorder associated with pulmonary disease (e.g. chronic  
obstructive pulmonary disease, cystic fibrosis, pulmonary thrombosis),  
neural disorders (e.g. Alzheimer's disease, Parkinson's disease,  
depression, psychoses), male reproductive disorders (e.g. male  
infertility, impotence, testicular cancer), heart defects (e.g.  
endocardial cushion defects, arrhythmia, myocardial ischaemia, myocardial  
infarction, pericardial effusion), hyperproliferative disorders,  
lymphoproliferative diseases; autoimmune disease (e.g. Addison's disease,  
multiple sclerosis, ophthalmia, diabetes mellitus), cancer, inflammation  
(e.g. graft versus host disease, chronic graft rejection), bacterial,  
fungal or parasitic infection (e.g. bacteraemia, endocarditis, whooping

cough, sepsis, food poisoning, pneumonia, wound infection, dysentery),  
vascular disorders and lymphatic disorders. This sequence represents the  
human HGPRBMV23 polypeptide

XX SQ Sequence 337 AA;  
Query Match 100.0%; Score 1771; DB 5; Length 337;  
Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDVAAPGNCNTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDVAAPGNCNTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPWKSTIIMLNACTDLYLTLSPFLIHYASGENWIFGDFMCKFIRSEHFNLYSS 120  
DB 61 KMRPWKSTIIMLNACTDLYLTLSPFLIHYASGENWIFGDFMCKFIRSEHFNLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
QY 181 SACLDLTSSDELTIKWYNLILTATFTFCLPLVIVTLCYTTIIHILTHGLQDSCCLKQKAR 240  
DB 181 SACLDLTSSDELTIKWYNLILTATFTFCLPLVIVTLCYTTIIHILTHGLQDSCCLKQKAR 240  
QY 241 RLTLILLAFVVCFLPFHILVIRIESLLISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTLILLAFVVCFLPFHILVIRIESLLISCSIEHQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 4  
ABB83819  
ID ABB83819 standard; protein; 337 AA.  
XX AC ABB83819;  
DT 18-SEP-2002 (first entry)  
XX Human P2Y-like receptor variant SEQ ID NO 4.  
XX Human; P2Y-like receptor; HIPHUM 0000037; immunity; inflammation; cancer;  
KW Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;  
KW immunomodulator; anti-inflammatory; cytostatic; antiasthmatic;  
KW gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide;  
KW antibacterial; immunosuppressive; dermatological; nephrotropic;  
KW antiallergic; analgesic; receptor.  
XX OS Homo sapiens.  
XX GB2369364-A.  
XX 29-MAY-2002.  
XX 31-AUG-2001; 2001GB-00021215.  
XX 01-SEP-2000; 2000GB-00021524.  
XX 06-SEP-2000; 2000GB-00021894.  
XX 25-SEP-2000; 2000GB-00023444.  
XX (GLAX ) GLAXO GROUP LTD.  
XX Foord SM, Ignar DM;  
XX WPI; 2002-511268/55.  
XX N-PSDB; ABB85630.  
XX An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can be  
PT used for the identification of agonists and antagonists which may be used

to treat an immune or inflammatory disease.

Claim 1; Page 30-31; 35pp; English.

The invention relates to an isolated P2Y-like receptor polypeptide (ABB83818-ABB83819) which is also referred to in the specification as HIPHUM 0000037. An effective amount of a substance (agonist or antagonist) which modulates P2Y receptor activity is useful to treat a subject having a disorder that is responsive to P2Y-like receptor modulation. The disorder is a disease of immunity or inflammation. The substance may also be used to manufacture a medicine for the treatment or prophylaxis of a disorder that is responsive to stimulation or modulation of P2Y-like receptor activity. Disorders which may be treated include colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome, gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative colitis, rheumatoid arthritis, viral diseases, bacterial infections, autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic rhinitis, inflammatory pain and general inflammation such as tendonitis, polymyositis or prostatitis. The invention provides alternative CC substances for the treatment of immunological and inflammatory diseases

Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.1e-194;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60  
QY 61 KMRPWKSTIIMNLACTDLYLTSPLLIHYASGENWIFGDFCKFIRESFHNLYSS 120  
DB 61 KMRPWKSTIIMNLACTDLYLTSPLLIHYASGENWIFGDFCKFIRESFHNLYSS 120  
QY 121 ILFTCTSPFYCVIIHPMSCFSIHKTRCAVAVCAVWVMSILVAVIPMTFLTSTNTR 180  
DB 121 ILFTCTSPFYCVIIHPMSCFSIHKTRCAVAVCAVWVMSILVAVIPMTFLTSTNTR 180  
QY 181 SACLDTSSDLNTIKWNLTLTATPCPLPVIIVTLCTVTIHTLTHGLQDSCCLKQKAR 240  
DB 181 SACLDTSSDLNTIKWNLTLTATPCPLPVIIVTLCTVTIHTLTHGLQDSCCLKQKAR 240  
QY 241 RLTIALLAFVCFPLPHILVRISRLLSISCSINQIHEAYIVSRPLAALNTFGNLL 300  
DB 241 RLTIALLAFVCFPLPHILVRISRLLSISCSINQIHEAYIVSRPLAALNTFGNLL 300  
QY 301 LYVVSDNFQAVCVTRCKVSGNLEQAKKISYNNP 337  
DB 301 LYVVSDNFQAVCVTRCKVSGNLEQAKKISYNNP 337

RESULT 5

ABG70271

ID ABG70271 standard; protein; 337 AA.

XX AC ABG70271;

XX AC ABG70271;

DT 05-NOV-2002 (first entry)

DE Human Purinoceptor-like protein.

XX Human; NOX; pathological condition; NOX-associated disorder;  
KW Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;  
KW pancreatitis; obesity; diabetes; autoimmune disease; infertility;  
KW renal artery stenosis; interstitial nephritis; glomerulonephritis;  
KW polycystic kidney disease; cataract; Alzheimer's disease; cancer;  
KW acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;  
KW congenital heart defect; scleroderma; endometriosis; haemophilia;  
KW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;  
KW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;  
KW acne; wound; asthma; human disease; calpain; epsin; zinc finger;  
KW low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;

KW

serine protease TLSP; mitogen activated protein kinase kinase-2;

glypican-2 precursor; thymosin beta-10.

XX Homo sapiens.

XX WO200255702-A2.

XX 18-JUL-2002.

XX 26-OCT-2001; 2001WO-US050925.

XX 26-OCT-2000; 2000US-0243320P.

XX 26-OCT-2000; 2000US-0243592P.

XX 26-OCT-2000; 2000US-0243642P.

XX 27-OCT-2000; 2000US-0243681P.

XX 27-OCT-2000; 2000US-0243863P.

XX 31-OCT-2000; 2000US-0244443P.

XX 01-NOV-2000; 2000US-0244995P.

XX 01-NOV-2000; 2000US-0245029P.

XX 02-NOV-2000; 2000US-0245293P.

XX 02-NOV-2000; 2000US-0245315P.

XX 02-NOV-2000; 2000US-0245316P.

XX 19-JAN-2001; 2001US-0262994P.

XX 15-FEB-2001; 2001US-0269056P.

XX 02-MAR-2001; 2001US-0272923P.

XX 15-MAR-2001; 2001US-0276565P.

XX 07-SEP-2001; 2001US-0318119P.

XX (CURA-) CURAGEN CORP.

XX Gangolli EA, Spytek KA, Gilbert J, Casman S, Blalock A, Li L;

Vernet CAM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;

Malyanankar U, Stone D, Millet I, Smithson G, Gunther E, Padigar M;

Taupier RJ, Anderson D;

XX WPI; 2002-590673/3.

XX N-PSDB; ABK51678.

XX Isolated NOX polypeptides and nucleic acid molecules useful for

treating, preventing, diagnosing and researching pathological conditions

in humans with a NOX-associated disorders, e.g. cancer, stroke or

Alzheimer's disease.

XX Claim 1; Page 32; 236pp; English.

XX The present invention relates to a new polypeptide that comprises any of

17 fully defined sequences of 43-990 amino acids given in the

specification. The NOX polypeptide, nucleic acid and antibody of the

invention are useful for treating or preventing a pathological condition

in humans with a NOX-associated disorder, e.g. Von Hippel-Lindau

syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,

diabetes, autoimmune disease, renal artery stenosis, interstitial

nephritis, glomerulonephritis, polycystic kidney disease, cataract,

Alzheimer's disease, acoustic trauma, cancer, infertility,

cardiomyopathies, atherosclerosis, hypertension, congenital heart

defects, scleroderma, endometriosis, haemophilia, dementia, stroke,

Parkinson's disease, Huntington's disease, epilepsy, multiple sclerosis,

anxiety, pain, leukaemias, hypothyroidism, psoriasis, acne, wounds and

asthma. They are also useful for the manufacture of a medicament for

treating a syndrome associated with a human disease, specifically a NOX-

associated disorder. They may also be useful in therapeutic applications

including protein therapy, as small molecule drug targets, as antibody

targets, as diagnostic and/or prognostic markers, in gene therapy, as

research tools and in tissue regeneration. The present amino acid

sequence represents one of the 17 novel proteins of the invention

XX Sequence 337 AA;

XX Query Match 100.0%; Score 1771; DB 5; Length 337;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-194;

XX Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60

QY



XX PR 14-AUG-2000; 2000US-0224989P.  
 XX PA (FARB ) BAYER AG.  
 XX PI Ramakrishnan S;  
 XX DR WPI; 2002-257607/30.  
 XX DR N-PSDB; ABK11381.  
 XX PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can be  
 PT regulated for treating infection, pain, cancer, diabetes, anorexia,  
 PT asthma, hypertension, neurological disorder and dyskinesia.  
 XX PS Claim 25; Fig 2; 118pp; English.  
 XX CC The invention relates to a purified human P2Y1-like G protein-coupled  
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it (including  
 CC 5' and 3' sequences, promoters, fragments, variants, or a sequence  
 CC encoding a protein at least 50% identical to the GPCR). Also included are  
 CC an expression vector comprising the nucleic acid, a host cell containing  
 CC the vector and the identification of modulators of the GPCR especially  
 CC those that reduce the activity of the GPCR. The nucleic acid is useful  
 CC for detecting a polynucleotide encoding the GPCR in a biological sample.  
 CC The GPCR and nucleic acid are useful for screening for agents which  
 CC decrease the activity of the GPCR and for modulators of the GPCR. The  
 CC modulator or agent useful for modulating the activity of P2Y1-like G  
 CC protein-coupled receptor in a disease such as bacterial, fungal,  
 CC protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma,  
 CC central nervous system (CNS) disease, acute heart failure, hypertension,  
 CC hyperextension, urinary retention, osteoporosis, diabetes, angina pectoris,  
 CC myocardial infarction, ulcer, inflammation, allergy, multiple sclerosis,  
 CC benign prostatic hypertrophy, psychotic and neurological disorders,  
 CC dyskinesias, HIV virus infection (human immunodeficiency virus), CNS  
 CC disorders such as Parkinson's disease, anxiety, schizophrenia, manic  
 CC depression, delirium, dementia, severe mental retardation, Huntington's  
 CC disease and Tourette's syndrome. The present sequence represents the P2Y1  
 CC -like GPCR of the invention  
 XX SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPKMHYLPVYIGLIFLVGPGNAVISTYIF 60  
 DB 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPKMHYLPVYIGLIFLVGPGNAVISTYIF 60  
 QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIKFSHFNLVSS 120  
 DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIKFSHFNLVSS 120  
 QY 121 ILELTCFSIFRYCVIIHPMCSFISIKTKCAVAVVWIIISLVAVIPMTLITSTNTR 180  
 DB 121 ILELTCFSIFRYCVIIHPMCSFISIKTKCAVAVVWIIISLVAVIPMTLITSTNTR 180  
 QY 181 SACLDTSSDELNTIKWNLIIITATTCFLPLVITLCVYIIHTLTHGLQDSCIKQKAR 240  
 DB 181 SACLDTSSDELNTIKWNLIIITATTCFLPLVITLCVYIIHTLTHGLQDSCIKQKAR 240  
 QY 241 RLTIILLAFVCFPLPHILRVIRIESRLLSISCIENQIHEAVIVSRPLAALNTFGNLL 300  
 DB 241 RLTIILLAFVCFPLPHILRVIRIESRLLSISCIENQIHEAVIVSRPLAALNTFGNLL 300  
 QY 301 LYVVSDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337  
 DB 301 LYVVSDNFQAVCSVTRCKVSGNLEQAKKISYNNP 337

RESULT 8  
 1. AAE21803  
 ID AAE21803 standard; protein; 337 AA.

XX AC AAE21803;  
 XX DT 16-JUL-2002 (first entry)  
 XX DE Human AXOR89 (G-protein coupled receptor) protein.  
 XX KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;  
 KW infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;  
 KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;  
 KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;  
 KW myocardial infarction; allergy; benign prostatic hypertrophy; migraine;  
 KW vomiting; psychotic; neurological disorder; anxiety; manic depression;  
 KW delirium; Huntington's Disease; Gilles de la Tourette's syndrome;  
 KW dementia; dyskinesia.  
 XX OS Homo sapiens.  
 XX FN GB2365012-A.  
 XX PD 13-FEB-2002.  
 XX PF 10-MAY-2001; 2001GB-00011437.  
 XX PR 11-MAY-2000; 2000US-00569137.  
 XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Elshourbagy N, Shabon U;  
 XX WPI; 2002-332558/37.  
 XX N-PSDB; AAD34278.  
 XX PT Novel AXOR89 polypeptide and polynucleotide encoding it, useful for  
 PT identifying agonists and antagonists in the treatment of diseases  
 XX associated with an AXOR89 imbalance, such as cancers, diabetes or asthma.  
 XX PS Claim 1; Page 30; 37pp; English.

CC The invention relates to an isolated AXOR89 polypeptide (G-protein  
 CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide  
 CC and polynucleotide encoding the polypeptide, is useful for identifying  
 CC agonists and antagonists (or inhibitors) that are potentially useful in  
 CC treating conditions associated with an AXOR89 imbalance, such as  
 CC bacterial, fungal or protozoan infections, cancers, pain, asthma,  
 CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart  
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,  
 CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign  
 CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological  
 CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,  
 CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's  
 CC syndrome. The polynucleotide sequence may also be used for chromosome  
 CC localisation or tissue expression studies. The AXOR89 is used as a  
 CC vaccine or to produce fusion proteins. The present sequence is human  
 CC AXOR89 protein  
 XX SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPKMHYLPVYIGLIFLVGPGNAVISTYIF 60  
 DB 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPKMHYLPVYIGLIFLVGPGNAVISTYIF 60  
 QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIKFSHFNLVSS 120  
 DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIKFSHFNLVSS 120  
 QY 121 ILELTCFSIFRYCVIIHPMCSFISIKTKCAVAVVWIIISLVAVIPMTLITSTNTR 180  
 DB 121 ILELTCFSIFRYCVIIHPMCSFISIKTKCAVAVVWIIISLVAVIPMTLITSTNTR 180

Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
QY 181 SACLDTSSDELNTIKWNLILTATTCFLPLVITLCTYTIHTLTHGLQTSCLKQKAR 240  
Db 181 SACLDTSSDELNTIKWNLILTATTCFLPLVITLCTYTIHTLTHGLQTSCLKQKAR 240  
QY 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNFTGNLL 300  
Db 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNFTGNLL 300  
QY 301 LYVVSDNFQQAQVCTVRCKVSGNLEQAQKISYNNP 337  
Db 301 LYVVSDNFQQAQVCTVRCKVSGNLEQAQKISYNNP 337  
RESULT 9  
ABP95602  
ID ABP95602 standard; protein; 337 AA.  
XX AC ABP95602;  
XX 06-MAR-2003 (first entry)  
XX Human GPCR polypeptide SEQ ID NO 14.  
DE Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
KW drug development; gustatory; taste; fragrance; receptor.  
XX Homo sapiens.  
OS  
XX WO200216548-A2.  
XX 28-FEB-2002.  
XX 30-JUL-2001; 2001WO-IB001446.  
XX 04-AUG-2000; 2000JP-00237818.  
XX 13-FEB-2001; 2001JP-00034434.  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
XX Haga T, Takeda S, Mitaku S;  
XX WPI; 2002-304118/34.  
XX N-PSDB; AB242876.  
XX Database global search for G protein-coupled receptors, proteins and  
PT encoded genes for studying in vivo signal transduction mechanism and  
PT identifying targets for drug development.  
XX  
XX Claim 10; SEQ ID NO 14; 97pp + Sequence Listing; Japanese.  
XX  
XX The invention relates to a method for screening G protein-coupled  
CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-  
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane  
CC domains with 250-1000 amino acid residues to give a gene homologous with  
CC a known GPCR gene. The receptor proteins and encoded genes are useful for  
CC studying in vivo signal transduction mechanism and identifying targets  
CC for drug development e.g. based on olfactory and gustatory receptors in  
CC form of agonists and antagonists by screening intrinsic and extrinsic  
CC ligands as bitter taste inhibitors, taste enhancers and fragrance  
CC improvers. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
XX Sequence 337 AA;  
SQ  
Query Match 100.0%; Score 1771; DB 5; Length 337;  
Best Local Similarity 100.0%; Pred No. 1.1e-194;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNEPLDYLANASDFPDYAAAFGNCNTDENIPLKMHYLPVIYGIIFLVGFFGNVISTYIF 60  
|||||

Db 1 MNEPLDYLANASDFPDYAAAFGNCNTDENIPLKMHYLPVIYGIIFLVGFFGNVISTYIF 60  
QY 61 KMRPKWSTIIMNLACTDLYLTSLPFLIHVYASGENWIFGDMCKFRFSPHENLYSS 120  
Db 61 KMRPKWSTIIMNLACTDLYLTSLPFLIHVYASGENWIFGDMCKFRFSPHENLYSS 120  
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNR 180  
QY 181 SACLDTSSDELNTIKWNLILTATTCFLPLVITLCTYTIHTLTHGLQTSCLKQKAR 240  
Db 181 SACLDTSSDELNTIKWNLILTATTCFLPLVITLCTYTIHTLTHGLQTSCLKQKAR 240  
QY 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNFTGNLL 300  
Db 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNFTGNLL 300  
QY 301 LYVVSDNFQQAQVCTVRCKVSGNLEQAQKISYNNP 337  
Db 301 LYVVSDNFQQAQVCTVRCKVSGNLEQAQKISYNNP 337  
RESULT 10  
AAO15399  
ID AAO15399 standard; protein; 337 AA.  
XX AC AAO15399;  
XX 27-SEP-2002 (first entry)  
XX Human G protein-coupled receptor.  
DE Human; gene therapy; G protein-coupled receptor; drug development;  
KW central nervous system disease; endocrine disease; metabolic disease;  
KW cancer; respiratory disease; digestive disease; immune disease;  
XX inflammation; infection; circulatory disease.  
OS Homo sapiens.  
XX WO200257441-A1.  
XX 25-JUL-2002.  
XX 17-JAN-2002; 2002WO-JP000270.  
XX 18-JAN-2001; 2001JP-00010714.  
XX 30-MAR-2001; 2001JP-00102484.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Miwa M, Ito T, Shintani Y, Miyajima N;  
XX WPI; 2002-566800/60.  
XX N-PSDB; AAL43942.  
XX Human kidney-originated G protein-coupled receptor protein TGR30 and  
PT encoded DNA, for developing drugs to treat central nervous diseases,  
PT endocrine diseases, metabolic diseases and cancer, including gene  
PT therapy.  
XX Claim 1; Page 88-90; 98pp; Japanese.  
XX The invention comprises the amino acid and coding sequence of a human G  
CC protein-coupled receptor. The DNA and protein sequences of the invention  
CC are useful for developing drugs to prevent or treat (gene therapy):  
CC central nervous system diseases; endocrine diseases; metabolic diseases;  
CC cancer; respiratory diseases; digestive diseases; immune diseases;  
CC inflammations; infections; and circulatory diseases. The present amino  
CC acid sequence represents the human G protein-coupled receptor of the  
XX invention  
XX Sequence 337 AA;  
SQ

```
Query Match      100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
Qy 61 KMRPKWSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKEIRSFHFNLYSS 120
Db 61 KMRPKWSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKEIRSFHFNLYSS 120
Qy 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAVIPMTFLTITSTNRTNR 180
Qy 181 SACDLTSSDELTNTKWNLLITATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCCLKOKAR 240
Db 181 SACDLTSSDELTNTKWNLLITATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCCLKOKAR 240
Qy 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
Db 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
Qy 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYSNNP 337
Db 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 11
ABB79438
ID ABB79438 standard; protein; 337 AA.
AC ABB79438;
XX
DT 05-JUL-2002 (first entry)
DE Human P2Y1-li.
KW Human; P2Y1-li; G protein-coupled; receptor; gene therapy; thyroid.
OS Homo sapiens.
XX
XX DE10046970-A1.
XX
XX 11-APR-2002.
XX
XX 22-SEP-2000; 2000DE-01046970.
XX
XX 22-SEP-2000; 2000DE-01046970.
XX
XX (BRUE/) BRUESS M.
XX (BOEN/) BOENISCH H.
XX
XX Bruess M, Boenisch H;
XX
XX WPI; 2002-353329/39.
XX
XX N-PSDB; ABL56197.
XX
XX New human P2Y1li gene, useful for treatment and diagnosis of associated
XX diseases, and related proteins, antibodies and modulators, encodes G
XX protein-coupled receptor.
XX
XX Claim 4; Page 3; 5pp; German.
XX
XX The invention relates to the human P2Y1li gene (I), including its 5' and
XX 3' untranslated regions, located on chromosome 13 and encoding a G
XX protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies
XX etc., are used for diagnosis and (gene) therapy of diseases that are
XX (in)directly associated with (I) or its expression products. No diseases
XX are specified but as (I) is expressed only in thyroid tissue, (I) is
XX presumed to be involved in regulation of thyroid function. The present
XX
```

```
CC sequence is that of P2Y1li
SQ Sequence 337 AA;

Query Match      100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
Qy 61 KMRPKWSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKEIRSFHFNLYSS 120
Db 61 KMRPKWSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKEIRSFHFNLYSS 120
Qy 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAVIPMTFLTITSTNRTNR 180
Qy 181 SACDLTSSDELTNTKWNLLITATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCCLKOKAR 240
Db 181 SACDLTSSDELTNTKWNLLITATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCCLKOKAR 240
Qy 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
Db 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
Qy 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYSNNP 337
Db 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 12
ABB81902
ID ABB81902 standard; protein; 337 AA.
XX
XX AC ABB81902;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human G-protein coupled receptor PFI-019.
XX
XX Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
XX anti-inflammatory; cytostatic; cardiovascular; antiallergic; hypotensive;
XX antiarteriosclerotic; osteopathic; hypertension; asthma;
XX arteriosclerosis.
XX
XX OS Homo sapiens.
XX
XX EP1219638-A2.
XX
XX 03-JUL-2002.
XX
XX 04-DEC-2001; 2001EP-00310136.
XX
XX 18-DEC-2000; 2000GB-00030854.
XX
XX 04-MAY-2001; 2001GB-00011031.
XX
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX
XX Fidock MD;
XX
XX WPI; 2002-521945/56.
XX N-PSDB; ABQ78847.
XX
XX New G-protein coupled receptor (GPCR) polypeptide with homology to P2Y
XX purinoreceptor, useful for treating e.g. inflammation or cancers in a
XX patient, or for screening GPCR agonists or antagonists for treating these
XX diseases.
XX
XX Claim 11; Fig 2; 19pp; English.
XX
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XX CC The invention relates to a novel G-protein coupled receptor (GPCR), and
CC CC the polynucleotide encoding it. The protein of the invention has
CC CC neuroprotective, anti-inflammatory, cytostatic, cardiovascular,
CC CC anti-allergic, hypotensive, anti-arteriosclerotic, and osteopathic
CC CC activity. The GPCR polypeptide is useful for manufacturing a medicament
CC CC for treating a patient who needs to upregulate a receptor. Preferably,
CC CC therapeutically useful areas are hypertension, asthma, and
CC CC atherosclerosis. The sequence represents the G-protein coupled receptor
CC CC of the invention, PFI-019
XX SQ Sequence 337 AA;
    Query Match          100.0%; Score 1771; DB 5; Length 337;
    Best Local Similarity 100.0%; Pred. No. 1.le-194;
    Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
    Db 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
    QY 61 KMRPKSSTIIMLNACTDILYLSLPFLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120
    Db 61 KMRPKSSTIIMLNACTDILYLSLPFLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120
    QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
    Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
    QY 181 SACLDTSSDELNTIKWNLLITATTPCLPLVIVTLVCTTTIHTLTHGLQDSCCLKQKAR 240
    Db 181 SACLDTSSDELNTIKWNLLITATTPCLPLVIVTLVCTTTIHTLTHGLQDSCCLKQKAR 240
    QY 241 RLTIILLAFVVCFLPFIHLVIRIESRLISTSCSIEHQIHEAYIVSRPLAALNTFGNLL 300
    Db 241 RLTIILLAFVVCFLPFIHLVIRIESRLISTSCSIEHQIHEAYIVSRPLAALNTFGNLL 300
    QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYSNNP 337
    Db 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYSNNP 337
    RESULT 13
    ID ABG70287 standard; protein; 337 AA.
    AC ABG70287;
    XX 21-OCT-2002 (first entry)
    DE Human novel polypeptide #3.
    KW Human; trauma; viral infection; parasitic infection; addiction;
    KW bacterial infection; Alzheimer's disease; Huntington's disease; anxiety;
    KW Parkinson's disease; behavioural disorder; pain; hair growth disease;
    KW alopecia; pigmentation disorder; inflammatory disorder; arthritis; AIDS;
    KW inflammatory bowel disease; Crohn's disease; cancer; adenocarcinoma;
    KW acquired immunodeficiency syndrome; colon; asthma; hypertension; obesity;
    KW autoimmune disease; diabetes; graft versus host disease; ulcer; bulimia;
    KW anorexia; dementia; gene therapy.
    OS Homo sapiens.
    XX WO200257452-A2.
    XX 25-JUL-2002.
    XX 17-DEC-2001; 2001WO-US049122.
    XX 15-DEC-2000; 2000US-0256025P.
    PR 30-JAN-2001; 2001US-0265163P.
    PR 02-MAR-2001; 2001US-0272929P.
    PR 09-MAR-2001; 2001US-0274864P.

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PR 16-MAR-2001; 2001US-0276688P.
PR 22-MAR-2001; 2001US-0277880P.
PR 25-APR-2001; 2001US-0286409P.
PR 31-JUL-2001; 2001US-0309246P.
PR 29-AUG-2001; 2001US-0315600P.
XX (CURA-) CURAGEN CORP.
XX Shimkets RT, Colman SD, Spytek KA, Ballinger RA, Guo X;
PI Tchernev VT, Shenoy SG, Li L, Ellerman KE, Zerhusen BD;
PI Patturajan M, Casman SJ, Boldog F, Gusev VY, Burgess CE, Edinger S;
PI Gangolli EA, Malyankar UM, Gunther E, Smithson G, Millet I;
PI Gerlach VL;
XX WPI; 2002-590743/63.
DR N-PSDB; ABS51730.
XX Novel polypeptide, designated NOVX for treating or preventing disorders
XX or symptoms e.g. trauma, Alzheimer's disease, cancers, acquired
XX immunodeficiency syndrome, asthma and rheumatoid arthritis.
XX Claim 1; Page 25; 252pp; English.
XX The invention relates to human novel polynucleotides and polypeptides.
XX The sequences are useful for the treatment, prevention and diagnosis of
XX disorders such as trauma, viral/parasitic/bacterial infections,
XX Alzheimer's disease, Huntington's disease, Parkinson's disease,
XX behavioural disorders, anxiety, addiction, pain, hair growth diseases,
XX alopecia, pigmentation disorder, inflammatory disorders such as osteo-
XX and rheumatoid arthritis, inflammatory bowel disease, Crohn's disease,
XX acquired immunodeficiency syndrome (AIDS), cancers such as colon cancer,
XX and adenocarcinoma, asthma, hypertension, autoimmune disease, diabetes,
XX obesity, graft versus host disease, ulcer, bulimia, anorexia and
XX dementia. Sequences ABG70285-ABG70305 represent human novel polypeptides
XX of the invention
XX SQ Sequence 337 AA;
    Query Match          100.0%; Score 1771; DB 5; Length 337;
    Best Local Similarity 100.0%; Pred. No. 1.le-194;
    Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
    Db 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
    QY 61 KMRPKSSTIIMLNACTDILYLSLPFLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120
    Db 61 KMRPKSSTIIMLNACTDILYLSLPFLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120
    QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
    Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
    QY 181 SACLDTSSDELNTIKWNLLITATTPCLPLVIVTLVCTTTIHTLTHGLQDSCCLKQKAR 240
    Db 181 SACLDTSSDELNTIKWNLLITATTPCLPLVIVTLVCTTTIHTLTHGLQDSCCLKQKAR 240
    QY 241 RLTIILLAFVVCFLPFIHLVIRIESRLISTSCSIEHQIHEAYIVSRPLAALNTFGNLL 300
    Db 241 RLTIILLAFVVCFLPFIHLVIRIESRLISTSCSIEHQIHEAYIVSRPLAALNTFGNLL 300
    QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYSNNP 337
    Db 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYSNNP 337
    RESULT 14
    ID ABP71377
    XX ABP71377 standard; protein; 337 AA.
    AC ABP71377;
    XX

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28-APR-2003 (first entry)  
Human TGR164 protein.  
G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343; TGR358; antitachycardic; neuroprotective; cerebroprotective; nephroprotective; anticonvulsant; hypotensive; hepatotropic; dermatological; human; immunosuppressive; antiinflammatory.  
Homo sapiens.  
W02003004678-A2.  
16-JAN-2003.  
01-JUL-2002; 2002WO-US020860.  
03-JUL-2001; 2001US-0302800P.  
(TULA-) TULARIK INC.  
Tian H, Dai K, Chen J, Zhao J, Cutler G;  
WPI; 2003-210368/20.  
DR N-PSDB; ABZ59170.  
New G-protein coupled receptor polypeptides designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs for treating or preventing e.g. asthma, multiple sclerosis, stroke or nephrolithiasis.  
Claim 17; Page 61; 74pp; English.  
The invention provides new G-protein coupled receptor (GPCR) polypeptides designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding polynucleotides. The polypeptides can be expressed by standard DNA recombination methodology. The polypeptides are useful for screening or identifying modulators of GPCR or signal transduction. The modulators of signal transduction are useful for treating or preventing TGR-associated disorders, e.g. asthma, multiple sclerosis or kidney disease. The polypeptides are useful as targets for diagnosing or treating e.g. epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia, asymptomatic urinary abnormalities, hypertension, nephrolithiasis, cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute inflammatory dermatoses. The present sequence represents a human TGR164 protein  
Sequence 337 AA;  
Query Match 100.0%; Score 1771; DB 6; Length 337;  
Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNEPLDYANASDPDYAAAFNGCTDNIPDKMYLPIVYIGIIFLVGPGNAVVISYIF 60  
DB 1 MNEPLDYANASDPDYAAAFNGCTDNIPDKMYLPIVYIGIIFLVGPGNAVVISYIF 60  
QY 61 KMRPWKSTIIMLNACTDILLYLTLPLHYVAGSNGWIFGDFMCKFIKPSHFHLYSS 120  
DB 61 KMRPWKSTIIMLNACTDILLYLTLPLHYVAGSNGWIFGDFMCKFIKPSHFHLYSS 120  
QY 121 ILFLTCSIFRYCVIHPMCSFISHKTRCAVACAVVWIIISLNAVIMPTFLTSTNTR 180  
DB 121 ILFLTCSIFRYCVIHPMCSFISHKTRCAVACAVVWIIISLNAVIMPTFLTSTNTR 180  
QY 181 SACLDTSSDELNTIKWYNILITATTCFLPIVITLCYIIHITLHGLTDCSLKQAR 240  
DB 181 SACLDTSSDELNTIKWYNILITATTCFLPIVITLCYIIHITLHGLTDCSLKQAR 240  
QY 241 RLTIILLALFVVCPLPHILRVIRIESRLISCSIEHQHEAVIVSRPLAALNTFGNLL 300  
DB 241 RLTIILLALFVVCPLPHILRVIRIESRLISCSIEHQHEAVIVSRPLAALNTFGNLL 300

301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337  
|||||  
301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337  
|||||  
RESULT 15  
ADC26010  
ID ADC26010 standard; protein; 337 AA.  
XX  
AC ADC26010;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human purinergic receptor P2Y-related GPCR10 alternative protein.  
XX  
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;  
KW anorectic; cardiant; hypotensive; osteopathic; antianginal;  
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;  
KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;  
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;  
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;  
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;  
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;  
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;  
KW human; GPCR10; purinergic receptor P2Y; chromosome 13.  
XX  
OS Homo sapiens.  
XX  
PN US2003088080-A1.  
XX  
PD 08-MAY-2003.  
XX  
XX 21-JUN-2001; 2001US-00885453.  
XX  
PR 20-JUN-2000; 2000US-0212908P.  
PR 05-DEC-2000; 2000EP-00870289.  
XX  
XX (COMM//) COMMUNI D.  
XX (LANN//) LANNON V.  
XX (GOVA//) GOVAERTS C.  
XX (PARW//) PARMENTIER M.  
XX (DETH//) DETHHEUX M.  
XX  
XX Communi D, Lannoy V, Govaerts C, Parmentier M, Dethheux M;  
WPI; 2003-657983/62.  
DR N-PSDB; ADC25997.  
XX  
XX New human G-protein coupled receptor, useful for treating receptor-mediated disorders, e.g. infections, cancer, pain, diabetes, obesity, acute heart failure, osteoporosis, stroke, ulcer, allergy, or neurological disorders.  
XX  
PS Claim 6; Page 15; 24pp; English.  
XX  
XX The invention relates to a novel G-protein coupled receptor (GPCR). The receptor, polynucleotide, agonist, reverse agonist and antagonist of the invention may be useful for treating receptor-mediated disorders including viral, fungal or bacterial infections, immune-related disorders such as cancer, pain, diabetes, obesity, anorexia, acute heart failure, hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke, ulcer and allergy, as well as psychotic and neurological disorders such as schizophrenia and dementia, degenerative diseases such as Parkinson's disease and Alzheimer's disease and dyskinesias such as Huntington's disease. The current sequence is that of the human purinergic receptor P2Y-related GPCR10 alternative protein of the invention which is encoded by DNA located on chromosome 13.  
XX  
SQ Sequence 337 AA;  
Query Match 100.0%; Score 1771; DB 7; Length 337;  
Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MNEPDLANASDPDYAAAFNGCTDENIPDKHYPVYIYGIIFLVGPGNAVVIYIF 60
Db 1 MNEPDLANASDPDYAAAFNGCTDENIPDKHYPVYIYGIIFLVGPGNAVVIYIF 60
Qy 61 KMRPWKSTIIIMNLACTDILLYLTSLPFLIHYASGENWIFGDMCKFIRFSHFNYSS 120
Db 61 KMRPWKSTIIIMNLACTDILLYLTSLPFLIHYASGENWIFGDMCKFIRFSHFNYSS 120
Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNRTNR 180
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNRTNR 180
Qy 181 SACLDLTSSDELNTIKWYNLILTATTCLPLVIVTLCYTTIIHTLTHGLQDSCCLKOKAR 240
Db 181 SACLDLTSSDELNTIKWYNLILTATTCLPLVIVTLCYTTIIHTLTHGLQDSCCLKOKAR 240
Qy 241 RLTIILLALLAFVVCPLPHILRVIRIESRLISCSISQIENQIHEAYIVSRPLAALNTFGNLL 300
Db 241 RLTIILLALLAFVVCPLPHILRVIRIESRLISCSISQIENQIHEAYIVSRPLAALNTFGNLL 300
Qy 301 LYVVSDNFQOAVGSTVRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVSDNFQOAVGSTVRCKVSGNLEQAKKISYNNP 337

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Search completed: October 29, 2004, 15:01:15  
 Job time : 163 secs

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